HUMAN xiap

```
       gaaaaggtggacaagtcctaatttcaagagaagatgacttttaacagttttgaaggatct
     1 ---------+---------+---------+---------+---------+---------+ 60

a                                       M  T  F  N  S  F  E  G  S    -

       aaaacttgtgtacctgcagacatcaataaggaagaagaatttgtagaagagtttaataga
    61 ---------+---------+---------+---------+---------+---------+ 120

a      K  T  C  V  P  A  D  I  N  K  E  E  E  F  V  E  E  F  N  R    -

       ttaaaaacttttgctaattttccaagtggtagtcctgtttcagcatcaacactggcacga
   121 ---------+---------+---------+---------+---------+---------+ 180

a      L  K  T  F  A  N  F  P  S  G  S  P  V  S  A  S  T  L  A  R    -

       gcagggtttctttatactggtgaaggagataccgtgcggtgctttagttgtcatgcagct
   181 ---------+---------+---------+---------+---------+---------+ 240

a      A  G  F  L  Y  T  G  E  G  D  T  V  R  C  F  S  C  H  A  A    -

       gtagatagatggcaatatggagactcagcagttggaagacacaggaaagtatccccaaat
   241 ---------+---------+---------+---------+---------+---------+ 300

a      V  D  R  W  Q  Y  G  D  S  A  V  G  R  H  R  K  V  S  P  N    -

       tgcagatttatcaacggcttttatcttgaaaatagtgccacgcagtctacaaattctggt
   301 ---------+---------+---------+---------+---------+---------+ 360

a      C  R  F  I  N  G  F  Y  L  E  N  S  A  T  Q  S  T  N  S  G    -
```

FIG. 1 (PAGE 1 OF 7)

HUMAN xiap

```
            atccagaatggtcagtacaaagttgaaaactatctgggaagcagagatcattttgcctta
      361   ---------+---------+---------+---------+---------+---------+  420

a           I  Q  N  G  Q  Y  K  V  E  N  Y  L  G  S  R  D  H  F  A  L   -

            gacaggccatctgagacacatgcagactatcttttgagaactgggcaggttgtagatata
      421   ---------+---------+---------+---------+---------+---------+  480

a           D  R  P  S  E  T  H  A  D  Y  L  L  R  T  G  Q  V  V  D  I   -

            tcagacaccatatacccgaggaaccctgccatgtattgtgaagaagctagattaaagtcc
      481   ---------+---------+---------+---------+---------+---------+  540

a           S  D  T  I  Y  P  R  N  P  A  M  Y  C  E  E  A  R  L  K  S   -

            tttcagaactggccagactatgctcacctaaccccaagagagttagcaagtgctggactc
      541   ---------+---------+---------+---------+---------+---------+  600

a           F  Q  N  W  P  D  Y  A  H  L  T  P  R  E  L  A  S  A  G  L   -

            tactacacaggtattggtgaccaagtgcagtgcttttgttgtggtggaaaactgaaaaat
      601   ---------+---------+---------+---------+---------+---------+  660

a           Y  Y  T  G  I  G  D  Q  V  Q  C  F  C  C  G  G  K  L  K  N   -

            tgggaaccttgtgatcgtgcctggtcagaacacaggcgacactttcctaattgcttcttt
      661   ---------+---------+---------+---------+---------+---------+  720

a           W  E  P  C  D  R  A  W  S  E  H  R  R  H  F  P  N  C  F  F   -
```

FIG. 1 (PAGE 2 OF 7)

HUMAN xiap

```
          gttttgggccggaatcttaatattcgaagtgaatctgatgctgtgagttctgataggaat
     721  ---------+---------+---------+---------+---------+---------+ 780

a         V  L  G  R  N  L  N  I  R  S  E  S  D  A  V  S  S  D  R  N  -

          ttcccaaattcaacaaatcttccaagaaatccatccatggcagattatgaagcacggatc
     781  ---------+---------+---------+---------+---------+---------+ 840

a         F  P  N  S  T  N  L  P  R  N  P  S  M  A  D  Y  E  A  R  I  -

          tttacttttgggacatggatatactcagttaacaaggagcagcttgcaagagctggattt
     841  ---------+---------+---------+---------+---------+---------+ 900

a         F  T  F  G  T  W  I  Y  S  V  N  K  E  Q  L  A  R  A  G  F  -

          tatgctttaggtgaaggtgataaagtaaagtgctttcactgtggaggagggctaactgat
     901  ---------+---------+---------+---------+---------+---------+ 960

a         Y  A  L  G  E  G  D  K  V  K  C  F  H  C  G  G  G  L  T  D  -

          tggaagcccagtgaagacccttgggaacaacatgctaaatggtatccaggtgcaaatat
     961  ---------+---------+---------+---------+---------+---------+ 1020

a         W  K  P  S  E  D  P  W  E  Q  H  A  K  W  Y  P  G  C  K  Y  -

          ctgttagaacagaagggacaagaatatataaacaatattcatttaactcattcacttgag
    1021  ---------+---------+---------+---------+---------+---------+ 1080

a         L  L  E  Q  K  G  Q  E  Y  I  N  N  I  H  L  T  H  S  L  E  -
```

FIG. 1 (PAGE 3 OF 7)

HUMAN xiap

```
             gagtgtctggtaagaactactgagaaaacaccatcactaactagaagaattgatgatacc
       1081  ---------+---------+---------+---------+---------+---------+ 1140

a            E  C  L  V  R  T  T  E  K  T  P  S  L  T  R  R  I  D  D  T  -

             atcttccaaaatcctatggtacaagaagctatacgaatggggttcagtttcaaggacatt
       1141  ---------+---------+---------+---------+---------+---------+ 1200

a            I  F  Q  N  P  M  V  Q  E  A  I  R  M  G  F  S  F  K  D  I  -

             aagaaaataatggaggaaaaaattcagatatctgggagcaactataaatcacttgaggtt
       1201  ---------+---------+---------+---------+---------+---------+ 1260

a            K  K  I  M  E  E  K  I  Q  I  S  G  S  N  Y  K  S  L  E  V  -

             ctggttgcagatctagtgaatgctcagaaagacagtatgcaagatgagtcaagtcagact
       1261  ---------+---------+---------+---------+---------+---------+ 1320

a            L  V  A  D  L  V  N  A  Q  K  D  S  M  Q  D  E  S  S  Q  T  -

             tcattacagaaagagattagtactgaagagcagctaaggcgcctgcaagaggagaagctt
       1321  ---------+---------+---------+---------+---------+---------+ 1380

a            S  L  Q  K  E  I  S  T  E  E  Q  L  R  R  L  Q  E  E  K  L  -

             tgcaaaatctgtatggatagaaatattgctatcgttttgttccttgtggacatctagtc
       1381  ---------+---------+---------+---------+---------+---------+ 1440
```

FIG. 1 (PAGE 4 OF 7)

HUMAN xiap

```
a          C   K   I   C   M   D   R   N   I   A   I   V   F   V   P   C   G   H   L   V    -

           acttgtaaacaatgtgctgaagcagttgacaagtgtcccatgtgctacacagtcattact
     1441  ---------+---------+---------+---------+---------+---------+ 1500

a          T   C   K   Q   C   A   E   A   V   D   K   C   P   M   C   Y   T   V   I   T    -

           ttcaagcaaaaaattttatgtcttaatctaactctatagtaggcatgttatgttgttct
     1501  ---------+---------+---------+---------+---------+---------+ 1560

a          F   K   Q   K   I   F   M   S   *                                                -

           tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattccat
     1561  ---------+---------+---------+---------+---------+---------+ 1620

a                                                                                           -

           tagcatttgctaccaagtaggaaaaaaaatgtacatggcagtgttttagttggcaatata
     1621  ---------+---------+---------+---------+---------+---------+ 1680

a                                                                                           -

           atctttgaatttcttgatttttcagggtattagctgtattatccattttttttactgtta
     1681  ---------+---------+---------+---------+---------+---------+ 1740

a                                                                                           -

           tttaattgaaaccatagactaagaataagaagcatcatactataactgaacacaatgtgt
     1741  ---------+---------+---------+---------+---------+---------+ 1800

a                                                                                           -
```

FIG. 1 (PAGE 5 OF 7)

HUMAN xiap

```
             attcatagtatactgatttaatttctaagtgtaagtgaattaatcatctggattttttat
      1801   ---------+---------+---------+---------+---------+---------+ 1860
 a                                                                         -

             tcttttcagataggcttaacaaatggagctttctgtatataaatgtggagattagagtta
      1861   ---------+---------+---------+---------+---------+---------+ 1920
 a                                                                         -

             atctccccaatcacataatttgttttgtgtgaaaaaggaataaattgttccatgctggtg
      1921   ---------+---------+---------+---------+---------+---------+ 1980
 a                                                                         -

             gaaagatagagattgtttttagaggttggttgttgtgttttaggattctgtccattttct
      1981   ---------+---------+---------+---------+---------+---------+ 2040
 a                                                                         -

             tgtaaagnnataaacacgnacntgtgcgaaatatntttgtaaagtgatttgccattnttg
      2041   ---------+---------+---------+---------+---------+---------+ 2100
 a                                                                         -

             aaagcgtatttaatgatagaatactatcgagccaacatgtactgacatggaaagatgtca
      2101   ---------+---------+---------+---------+---------+---------+ 2160
 a                                                                         -
```

FIG. 1 (PAGE 6 OF 7)

HUMAN xiap

```
          nagatatgttaagtgtaaaatgcaagtggcnnnacactatgtatagtctgagccagatca
     2161 ---------+---------+---------+---------+---------+---------+ 2220

a                                                                    -

          aagtatgtatgttnttaatatgcatagaacnanagatttggaaagatatacaccaaactg
     2221 ---------+---------+---------+---------+---------+---------+ 2280

a                                                                    -

          ttaaatgtggtttctcttcggggagggggggattgggggaggggccccagaggggtttta
     2281 ---------+---------+---------+---------+---------+---------+ 2340

a                                                                    -

          naggggccttttcactttcnacttttttcattttgttctgttcgnattttttataagtat
     2341 ---------+---------+---------+---------+---------+---------+ 2400

a                                                                    -

          gtanaccccnaagggttttatggnaactaacatcagtaacctaacccccgtgactatcct
     2401 ---------+---------+---------+---------+---------+---------+ 2460

a                                                                    -

          gtnctcttcctagggagctgtnttgtttcccacccaccacccttccctctgaacaaatgc
     2461 ---------+---------+---------+---------+---------+---------+ 2520

a                                                                    -

          ctgagtgctggggcactttn
     2521 ---------+---------+ 2540

a                           -
```

FIG. 1 (PAGE 7 OF 7)

HUMAN hiap-1

```
      TCCTTGAGATGTATCAGTATAGGATTTAGGATCTCCATGTTGGAACTCTAAATGCATAGA
    1 ---------+---------+---------+---------+---------+---------+ 60

c                                                                  -

      AATGGAAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAAAACTGATAAAA
   61 ---------+---------+---------+---------+---------+---------+ 120

c                                                                  -

      GCAAAGCCATGCACAAAACTACCTCCCTAGAGAAAGGCTAGTCCCTTTTCTTCCCCATTC
  121 ---------+---------+---------+---------+---------+---------+ 180

c                                                                  -

      ATTTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAATTTGATGAAAAGCGCCA
  181 ---------+---------+---------+---------+---------+---------+ 240

c             M  N  I  V  E  N  S  I  F  L  S  N  L  M  K  S  A  N -

      ACACGTTTGAACTGAAATACGACTTGTCATGTGAACTGTACCGAATGTCTACGTATTCCA
  241 ---------+---------+---------+---------+---------+---------+ 300

c       T  F  E  L  K  Y  D  L  S  C  E  L  Y  R  M  S  T  Y  S  T -

      CTTTTCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGCTGGTTTCTATTACA
  301 ---------+---------+---------+---------+---------+---------+ 360

c       F  P  A  G  V  P  V  S  E  R  S  L  A  R  A  G  F  Y  Y  T -
```

FIG. 2 (PAGE 1 OF 8)

HUMAN hiap-1

```
         CTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAAAA
     361 ---------+---------+---------+---------+---------+---------+ 420

c          G  V  N  D  K  V  K  C  F  C  C  G  L  M  L  D  N  W  K  R -

         GAGGAGACAGTCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTCGTTCAGA
     421 ---------+---------+---------+---------+---------+---------+ 480

c          G  D  S  P  T  E  K  H  K  K  L  Y  P  S  C  R  F  V  Q  S -

         GTCTAAATTCCGTTAACAACTTGGAAGCTACCTCTCAGCCTACTTTTCCTTCTTCAGTAA
     481 ---------+---------+---------+---------+---------+---------+ 540

c          L  N  S  V  N  N  L  E  A  T  S  Q  P  T  F  P  S  S  V  T -

         CACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATTTCCGTGGCTCTT
     541 ---------+---------+---------+---------+---------+---------+ 600

c          H  S  T  H  S  L  L  P  G  T  E  N  S  G  Y  F  R  G  S  Y -

         ATTCAAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAATTTTCTGCCTTGA
     601 ---------+---------+---------+---------+---------+---------+ 660

c          S  N  S  P  S  N  P  V  N  S  R  A  N  Q  E  F  S  A  L  M -

         TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTACTTACTTTTCAGA
     661 ---------+---------+---------+---------+---------+---------+ 720

c          R  S  S  Y  P  C  P  M  N  N  E  N  A  R  L  L  T  F  Q  T -
```

FIG. 2 (PAGE 2 OF 8)

HUMAN hiap-1

```
          CATGGCCATTGACTTTTCTGTCGCCAACAGATCTGGCACGAGCAGGCTTTTACTACATAG
     721  ---------+---------+---------+---------+---------+---------+ 780

c           W  P  L  T  F  L  S  P  T  D  L  A  R  A  G  F  Y  Y  I  G -

          GACCTGGAGACAGAGTGGCTTGCTTTGCCTGTGGTGGAAAATTGAGCAATTGGGAACCGA
     781  ---------+---------+---------+---------+---------+---------+ 840

c           P  G  D  R  V  A  C  F  A  C  G  G  K  L  S  N  W  E  P  K -

          AGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCATTTATAGAAAATC
     841  ---------+---------+---------+---------+---------+---------+ 900

c           D  N  A  M  S  E  H  L  R  H  F  P  K  C  P  F  I  E  N  Q -

          AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACACATGCAGCCC
     901  ---------+---------+---------+---------+---------+---------+ 960

c           L  Q  D  T  S  R  Y  T  V  S  N  L  S  M  Q  T  H  A  A  R -

          GCTTTAAAACATTCTTTAACTGGCCCTCTAGTGTTCTAGTTAATCCTGAGCAGCTTGCAA
     961  ---------+---------+---------+---------+---------+---------+ 1020

c           F  K  T  F  F  N  W  P  S  S  V  L  V  N  P  E  Q  L  A  S -

          GTGCGGGTTTTTATTATGTGGGTAACAGTGATGATGTCAAATGCTTTTGCTGTGATGGTG
    1021  ---------+---------+---------+---------+---------+---------+ 1080

c           A  G  F  Y  Y  V  G  N  S  D  D  V  K  C  F  C  C  D  G  G -
```

FIG. 2 (PAGE 3 OF 8)

HUMAN hiap-1

```
          GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGGTTTCCAA
     1081 ---------+---------+---------+---------+---------+---------+ 1140

c           L  R  C  W  E  S  G  D  D  P  W  V  Q  H  A  K  W  F  P  R -

          GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAGTTCAAGCCAGTT
     1141 ---------+---------+---------+---------+---------+---------+ 1200

c           C  E  Y  L  I  R  I  K  G  Q  E  F  I  R  Q  V  Q  A  S  Y -

          ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCAGGAGATGAAAATGCAG
     1201 ---------+---------+---------+---------+---------+---------+ 1260

c           P  H  L  L  E  Q  L  L  S  T  S  D  S  P  G  D  E  N  A  E -

          AGTCATCAATTATCCATTTGGAACCTGGAGAAGACCATTCAGAAGATGCAATCATGATGA
     1261 ---------+---------+---------+---------+---------+---------+ 1320

c           S  S  I  I  H  L  E  P  G  E  D  H  S  E  D  A  I  M  M  N -

          ATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAAACAGA
     1321 ---------+---------+---------+---------+---------+---------+ 1380

c           T  P  V  I  N  A  A  V  E  M  G  F  S  R  S  L  V  K  Q  T -

          CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCAATGATCTTGTGT
     1381 ---------+---------+---------+---------+---------+---------+ 1440

c           V  Q  R  K  I  L  A  T  G  E  N  Y  R  L  V  N  D  L  V  L -
```

FIG. 2 (PAGE 4 OF 8)

HUMAN hiap-1

```
          TAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAAGAGCAACTGAGG
     1441 ---------+---------+---------+---------+---------+---------+ 1500

c           D  L  L  N  A  E  D  E  I  R  E  E  E  R  E  R  A  T  E  E -

          AAAAAGAATCAAATGATTTATTATTAATCCGGAAGAATAGAATGGCACTTTTTCAACATT
     1501 ---------+---------+---------+---------+---------+---------+ 1560

c           K  E  S  N  D  L  L  L  I  R  K  N  R  M  A  L  F  Q  H  L -

          TGACTTGTGTAATTCCAATCCTGGATAGTCTACTAACTGCCGGAATTATTAATGAACAAG
     1561 ---------+---------+---------+---------+---------+---------+ 1620

c           T  C  V  I  P  I  L  D  S  L  L  T  A  G  I  I  N  E  Q  E -

          AACATGATGTTATTAAACAGAAGACACAGACGTCTTTACAAGCAAGAGAACTGATTGATA
     1621 ---------+---------+---------+---------+---------+---------+ 1680

c           H  D  V  I  K  Q  K  T  Q  T  S  L  Q  A  R  E  L  I  D  T -

          CGATTTTAGTAAAAGGAAATATTGCAGCCACTGTATTCAGAAACTCTCTGCAAGAAGCTG
     1681 ---------+---------+---------+---------+---------+---------+ 1740

c           I  L  V  K  G  N  I  A  A  T  V  F  R  N  S  L  Q  E  A  E -

          AAGCTGTGTTATATGAGCATTTATTTGTGCAACAGGACATAAAATATATTCCCACAGAAG
     1741 ---------+---------+---------+---------+---------+---------+ 1800

c           A  V  L  Y  E  H  L  F  V  Q  Q  D  I  K  Y  I  P  T  E  D -
```

FIG. 2 (PAGE 5 OF 8)

HUMAN hiap-1

```
           ATGTTTCAGATCTACCAGTGGAAGAACAATTGCGGAGACTACCAGAAGAAAGAACATGTA
      1801 ---------+---------+---------+---------+---------+---------+ 1860

c            V  S  D  L  P  V  E  E  Q  L  R  R  L  P  E  E  R  T  C  K -

           AAGTGTGTATGGACAAAGAAGTGTCCATAGTGTTTATTCCTTGTGGTCATCTAGTAGTAT
      1861 ---------+---------+---------+---------+---------+---------+ 1920

c            V  C  M  D  K  E  V  S  I  V  F  I  P  C  G  H  L  V  V  C -

           GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCTATTTGTAGGAGTACAATCAAGGGTA
      1921 ---------+---------+---------+---------+---------+---------+ 1980

c            K  D  C  A  P  S  L  R  K  C  P  I  C  R  S  T  I  K  G  T -

           CAGTTCGTACATTTCTTTCATGAAGAAGAACCAAAACATCGTCTAAACTTTAGAATTAAT
      1981 ---------+---------+---------+---------+---------+---------+ 2040

c            V  R  T  F  L  S  *                                         -

           TTATTAAATGTATTATAACTTTAACTTTTATCCTAATTTGGTTTCCTTAAAATTTTTATT
      2041 ---------+---------+---------+---------+---------+---------+ 2100

c                                                                        -

           TATTTACAACTCAAAAAACATTGTTTTGTGTAACATATTTATATATGTATCTAAACCATA
      2101 ---------+---------+---------+---------+---------+---------+ 2160

c                                                                        -
```

FIG. 2 (PAGE 6 OF 8)

HUMAN hiap-1

```
          TGAACATATATTTTTTAGAAACTAAGAGAATGATAGGCTTTTGTTCTTATGAACGAAAAA
     2161 ---------+---------+---------+---------+---------+---------+ 2220

c                                                                         -

          GAGGTAGCACTACAAACACAATATTCAATCCAAATTTCAGCATTATTGAAATTGTAAGTG
     2221 ---------+---------+---------+---------+---------+---------+ 2280

c                                                                         -

          AAGTAAAACTTAAGATATTTGAGTTAACCTTTAAGAATTTTAAATATTTTGGCATTGTAC
     2281 ---------+---------+---------+---------+---------+---------+ 2340

c                                                                         -

          TAATACCGGGAACATGAAGCCAGGTGTGGTGGTATGTACCTGTAGTCCCAGGCTGAGGCA
     2341 ---------+---------+---------+---------+---------+---------+ 2400

c                                                                         -

          AGAGAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATACTGAGACCCTGCC
     2401 ---------+---------+---------+---------+---------+---------+ 2460

c                                                                         -

          TTTAAAAACXAACAGXACCAAAXCCAAACACCAGGGACACATTTCTCTGTCTTTTTTGAT
     2461 ---------+---------+---------+---------+---------+---------+ 2520

c                                                                         -
```

FIG. 2 (PAGE 7 OF 8)

HUMAN hiap-1

```
       CAGTGTCCTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTAGGGACATGGTGT
  2521 ---------+---------+---------+---------+---------+---------+ 2580

c                                                                   -

       TTTTATAAAGAATTCTGTGAGXAAAAATTTAATAAAGCAACCXAAATTACTCTTAAAAAA
  2581 ---------+---------+---------+---------+---------+---------+ 2640

c                                                                   -

       AAAAAAAAAAAAAAAACTCGAGGGGCCCGTACCAAT
  2641 ---------+---------+---------+------ 2676

c                                     -
```

FIG. 2 (PAGE 8 OF 8)

HUMAN hiap-2

```
         TTAGGTTACCTGAAAGAGTTACTACAACCCCAAAGAGTTGTGTTCTAAGTAGTATCTTGG
       1 ---------+---------+---------+---------+---------+---------+ 60

   a                                                                -

         TAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAAAG
      61 ---------+---------+---------+---------+---------+---------+ 120

   a                                                                -

         TGTAGTAAATTCTACATAAGAGTCTATCATTGATTTCTTTTTGTGGTGGAAATCTTAGTT
     121 ---------+---------+---------+---------+---------+---------+ 180

   a                                                                -

         CATGTGAAGAAATTTCATGTGAATGTTTTAGCTATCAAACAGTACTGTCACCTACTCATG
     181 ---------+---------+---------+---------+---------+---------+ 240

   a                                                          M     -

         CACAAAACTGCCTCCCAAAGACTTTTCCCAGGTCCCTCGTATCAAAACATTAAGAGTATA
     241 ---------+---------+---------+---------+---------+---------+ 300

   a     H  K  T  A  S  Q  R  L  F  P  G  P  S  Y  Q  N  I  K  S  I -

         ATGGAAGATAGCACGATCTTGTCAGATTGGACAAACAGCAACAAACAAAAAATGAAGTAT
     301 ---------+---------+---------+---------+---------+---------+ 360

   a     M  E  D  S  T  I  L  S  D  W  T  N  S  N  K  Q  K  M  K  Y -
```

FIG. 3 (PAGE 1 OF 7)

HUMAN hiap-2

```
        GACTTTTCCTGTGAACTCTACAGAATGTCTACATATTCAACTTTCCCCGCCGGGGTGCCT
    361 ---------+---------+---------+---------+---------+---------+ 420

a       D  F  S  C  E  L  Y  R  M  S  T  Y  S  T  F  P  A  G  V  P   -

        GTCTCAGAAAGGAGTCTTGCTCGTGCTGGTTTTTATTATACTGGTGTGAATGACAAGGTC
    421 ---------+---------+---------+---------+---------+---------+ 480

a       V  S  E  R  S  L  A  R  A  G  F  Y  Y  T  G  V  N  D  K  V   -

        AAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAAACTAGGAGACAGTCCTATTCAA
    481 ---------+---------+---------+---------+---------+---------+ 540

a       K  C  F  C  C  G  L  M  L  D  N  W  K  L  G  D  S  P  I  Q   -

        AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAATCTGGTTTCAGCTAGTCTG
    541 ---------+---------+---------+---------+---------+---------+ 600

a       K  H  K  Q  L  Y  P  S  C  S  F  I  Q  N  L  V  S  A  S  L   -
        GGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATCTCCC
    601 ---------+---------+---------+---------+---------+---------+ 660

a       G  S  T  S  K  N  T  S  P  M  R  N  S  F  A  H  S  L  S  P   -

        ACCTTGGAACATAGTAGCTTGTTCAGTGGTTCTTACTCCAGCCTTCCTCCAAACCCTCTT
    661 ---------+---------+---------+---------+---------+---------+ 720

a       T  L  E  H  S  S  L  F  S  G  S  Y  S  S  L  P  P  N  P  L   -
```

FIG. 3 (PAGE 2 OF 7)

HUMAN hiap-2

```
          AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG
     721 ---------+---------+---------+---------+---------+---------+ 780

a         N  S  R  A  V  E  D  I  S  S  S  R  T  N  P  Y  S  Y  A  M   -

          AGTACTGAAGAAGCCAGATTTCTTACCTACCATATGTGGCCATTAACTTTTTTGTCACCA
     781 ---------+---------+---------+---------+---------+---------+ 840

a         S  T  E  E  A  R  F  L  T  Y  H  M  W  P  L  T  F  L  S  P   -

          TCAGAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCTTT
     841 ---------+---------+---------+---------+---------+---------+ 900

a         S  E  L  A  R  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C  F   -

          GCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAAGGATGATGCTATGTCAGAACACCGG
     901 ---------+---------+---------+---------+---------+---------+ 960

a         A  C  G  G  K  L  S  N  W  E  P  K  D  D  A  M  S  E  H  R   -

          AGGCATTTTCCCAACTGTCCATTTTTGGAAAATTCTCTAGAAACTCTGAGGTTTAGCATT
     961 ---------+---------+---------+---------+---------+---------+ 1020

a         R  H  F  P  N  C  P  F  L  E  N  S  L  E  T  L  R  F  S  I   -

          TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCATCT
    1021 ---------+---------+---------+---------+---------+---------+ 1080

a         S  N  L  S  M  Q  T  H  A  A  R  M  R  T  F  M  Y  W  P  S   -
```

FIG. 3 (PAGE 3 OF 7)

HUMAN hiap-2

```
          AGTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTTTATTATGTGGGTCGCAAT
     1081 ---------+---------+---------+---------+---------+---------+ 1140

a          S  V  P  V  Q  P  E  Q  L  A  S  A  G  F  Y  Y  V  G  R  N  -

          GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTTGGGAATCTGGAGATGAT
     1141 ---------+---------+---------+---------+---------+---------+ 1200

a          D  D  V  K  C  F  G  C  D  G  G  L  R  C  W  E  S  G  D  D  -

          CCATGGGTAGAACATGCCAAGTGGTTTCCAAGGTGTGAGTTCTTGATACGAATGAAAGGC
     1201 ---------+---------+---------+---------+---------+---------+ 1260

a          P  W  V  E  H  A  K  W  F  P  R  C  E  F  L  I  R  M  K  G  -

          CAAGAGTTTGTTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGTCA
     1261 ---------+---------+---------+---------+---------+---------+ 1320

a          Q  E  F  V  D  E  I  Q  G  R  Y  P  H  L  L  E  Q  L  L  S  -

          ACTTCAGATACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCATTTTGGACCTGGA
     1321 ---------+---------+---------+---------+---------+---------+ 1380

a          T  S  D  T  T  G  E  E  N  A  D  P  P  I  I  H  F  G  P  G  -

          GAAAGTTCTTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCTTGGAA
     1381 ---------+---------+---------+---------+---------+---------+ 1440

a          E  S  S  S  E  D  A  V  M  M  N  T  P  V  V  K  S  A  L  E  -
```

FIG. 3 (PAGE 4 OF 7)

HUMAN hiap-2

```
          ATGGGCTTTAATAGAGACCTGGTGAAACAAACAGTTCTAAGTAAAATCCTGACAACTGGA
     1441 ---------+---------+---------+---------+---------+---------+ 1500

a         M  G  F  N  R  D  L  V  K  Q  T  V  L  S  K  I  L  T  T  G   -

          GAGAACTATAAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAAAA
     1501 ---------+---------+---------+---------+---------+---------+ 1560

a         E  N  Y  K  T  V  N  D  I  V  S  A  L  L  N  A  E  D  E  K   -

          AGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTTGTCATTAATT
     1561 ---------+---------+---------+---------+---------+---------+ 1620

a         R  E  E  E  K  E  K  Q  A  E  E  M  A  S  D  D  L  S  L  I   -

          CGGAAGAACAGAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCTATCCTGGATAAT
     1621 ---------+---------+---------+---------+---------+---------+ 1680

a         R  K  N  R  M  A  L  F  Q  Q  L  T  C  V  L  P  I  L  D  N   -

          CTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAAACAAAAAACACAG
     1681 ---------+---------+---------+---------+---------+---------+ 1740

a         L  L  K  A  N  V  I  N  K  Q  E  H  D  I  I  K  Q  K  T  Q   -

          ATACCTTTACAAGCGAGAGAACTGATTGATACCATTTGGGTTAAAGGAAATGCTGCGGCC
     1741 ---------+---------+---------+---------+---------+---------+ 1800

a         I  P  L  Q  A  R  E  L  I  D  T  I  W  V  K  G  N  A  A  A   -
```

FIG. 3 (PAGE 5 OF 7)

HUMAN hiap-2

```
       AACATCTTCAAAAACTGTCTAAAAGAAATTGACTCTACATTGTATAAGAACTTATTTGTG
  1801 ---------+---------+---------+---------+---------+---------+ 1860

a      N  I  F  K  N  C  L  K  E  I  D  S  T  L  Y  K  N  L  F  V   -

       GATAAGAATATGAAGTATATTCCAACAGAAGATGTTTCAGGTCTGTCACTGGAAGAACAA
  1861 ---------+---------+---------+---------+---------+---------+ 1920

a      D  K  N  M  K  Y  I  P  T  E  D  V  S  G  L  S  L  E  E  Q   -

       TTGAGGAGGTTGCAAGAAGAACGAACTTGTAAAGTGTGTATGGACAAAGAAGTTTCTGTT
  1921 ---------+---------+---------+---------+---------+---------+ 1980

a      L  R  R  L  Q  E  E  R  T  C  K  V  C  M  D  K  E  V  S  V   -

       GTATTTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCCTTCTCTAAGAAAA
  1981 ---------+---------+---------+---------+---------+---------+ 2040

a      V  F  I  P  C  G  H  L  V  V  C  Q  E  C  A  P  S  L  R  K   -

       TGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTCGTACATTTCTCTCTTAAAGAAAA
  2041 ---------+---------+---------+---------+---------+---------+ 2100

a      C  P  I  C  R  G  I  I  K  G  T  V  R  T  F  L  S  *         -

       ATAGTCTATATTTTAACCTGCATAAAAAGGTCTTTAAAATATTGTTGAACACTTGAAGCC
  2101 ---------+---------+---------+---------+---------+---------+ 2160

a                                                                   -
```

FIG. 3 (PAGE 6 OF 7)

HUMAN hiap-2

```
        ATCTAAAGTAAAAAGGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCTGC
   2161 ---------+---------+---------+---------+---------+---------+ 2220

a                                                                        -

        TTTGGTACTAATAATCTTGTTTCTGAAAAGATGGTATCATATATTTAATCTTAATCTGTT
   2221 ---------+---------+---------+---------+---------+---------+ 2280

a                                                                        -

        TATTTACAAGGGAAGATTTATGTTTGGTGAACTATATTAGTATGTATGTGTACCTAAGGG
   2281 ---------+---------+---------+---------+---------+---------+ 2340

a                                                                        -

        AGTAGCGTCXCTGCTTGTTATGCATCATTTCAGGAGTTACTGGATTTGTTGTTCTTTCAG
   2341 ---------+---------+---------+---------+---------+---------+ 2400

a                                                                        -

        AAAGCTTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACTCTGGAGTT
   2401 ---------+---------+---------+---------+---------+---------+ 2460

a                                                                        -

        CATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAAATAAGGA
   2461 ---------+---------+---------+---------+---------+---------+ 2520

a                                                                        -

        TTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAAAG
   2521 ---------+---------+---------+---------+---------+---------+ 2580

a                                                                        -
```

FIG. 3 (PAGE 7 OF 7)

MOUSE xiap

```
        GACACTCTGCTGGGCGGCGGGCCGCCCTCCTCCGGGACCTCCCCTCGGAACCGTCGCCC
      1 ---------+---------+---------+---------+---------+---------+ 60

a                                                                      -

        GCGGCGCTTAGTTAGGACTGGAGTGCTTGGCGCGAAAAGGTGGACAAGTCCTATTTTCCA
     61 ---------+---------+---------+---------+---------+---------+ 120

a                                                                      -

        GAGAAGATGACTTTTAACAGTTTTGAAGGAACTAGAACTTTTGTACTTGCAGACACCAAT
    121 ---------+---------+---------+---------+---------+---------+ 180

a              M  T  F  N  S  F  E  G  T  R  T  F  V  L  A  D  T  N    -

        AAGGATGAAGAATTTGTAGAAGAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGT
    181 ---------+---------+---------+---------+---------+---------+ 240

a        K  D  E  E  F  V  E  E  F  N  R  L  K  T  F  A  N  F  P  S    -

        AGTAGTCCTGTTTCAGCATCAACATTGGCGCGAGCTGGGTTTCTTTATACCGGTGAAGGA
    241 ---------+---------+---------+---------+---------+---------+ 300

a        S  S  P  V  S  A  S  T  L  A  R  A  G  F  L  Y  T  G  E  G    -

        GACACCGTGCAATGTTTCAGTTGTCATGCGGCAATAGATAGATGGCAGTATGGAGACTCA
    301 ---------+---------+---------+---------+---------+---------+ 360

a        D  T  V  Q  C  F  S  C  H  A  A  I  D  R  W  Q  Y  G  D  S    -
```

FIG. 4 (PAGE 1 OF 6)

MOUSE xiap

```
         GCTGTTGGAAGACACAGGAGAATATCCCCAAATTGCAGATTTATCAATGGTTTTTATTTT
    361  ---------+---------+---------+---------+---------+---------+ 420

a        A  V  G  R  H  R  R  I  S  P  N  C  R  F  I  N  G  F  Y  F  -

         GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAATCTGAA
    421  ---------+---------+---------+---------+---------+---------+ 480

a        E  N  G  A  A  Q  S  T  N  P  G  I  Q  N  G  Q  Y  K  S  E  -

         AACTGTGTGGGAAATAGAAATCCTTTTGCCCCTGACAGGCCACCTGAGACTCATGCTGAT
    481  ---------+---------+---------+---------+---------+---------+ 540

a        N  C  V  G  N  R  N  P  F  A  P  D  R  P  P  E  T  H  A  D  -

         TATCTCTTGAGAACTGGACAGGTTGTAGATATTTCAGACACCATATACCCGAGGAACCCT
    541  ---------+---------+---------+---------+---------+---------+ 600

a        Y  L  L  R  T  G  Q  V  V  D  I  S  D  T  I  Y  P  R  N  P  -

         GCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCAT
    601  ---------+---------+---------+---------+---------+---------+ 660

a        A  M  C  S  E  E  A  R  L  K  S  F  Q  N  W  P  D  Y  A  H  -

         TTAACCCCCAGAGAGTTAGCTAGTGCTGGCCTCTACTACACAGGGGCTGATGATCAAGTG
    661  ---------+---------+---------+---------+---------+---------+ 720

a        L  T  P  R  E  L  A  S  A  G  L  Y  Y  T  G  A  D  D  Q  V  -
```

FIG. 4 (PAGE 2 OF 6)

MOUSE xiap

```
         CAATGCTTTTGTTGTGGGGGAAAACTGAAAAATTGGGAACCCTGTGATCGTGCCTGGTCA
     721 ---------+---------+---------+---------+---------+---------+ 780

a        Q  C  F  C  C  G  G  K  L  K  N  W  E  P  C  D  R  A  W  S   -

         GAACACAGGAGACACTTTCCCAATTGCTTTTTGTTTGGGCCGGAACGTTAATGTTCGA
     781 ---------+---------+---------+---------+---------+---------+ 840

a        E  H  R  R  H  F  P  N  C  F  F  V  L  G  R  N  V  N  V  R   -

         AGTGAATCTGGTGTGAGTTCTGATAGGAATTTCCCAAATTCAACAAACTCTCCAAGAAAT
     841 ---------+---------+---------+---------+---------+---------+ 900

a        S  E  S  G  V  S  S  D  R  N  F  P  N  S  T  N  S  P  R  N   -

         CCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTT
     901 ---------+---------+---------+---------+---------+---------+ 960

a        P  A  M  A  E  Y  E  A  R  I  V  T  F  G  T  W  I  Y  S  V   -

         AACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAG
     961 ---------+---------+---------+---------+---------+---------+ 1020

a        N  K  E  Q  L  A  R  A  G  F  Y  A  L  G  E  G  D  K  V  K   -

         TGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAG
    1021 ---------+---------+---------+---------+---------+---------+ 1080

a        C  F  H  C  G  G  G  L  T  D  W  K  P  S  E  D  P  W  D  Q   -
```

FIG. 4 (PAGE 3 OF 6)

MOUSE xiap

```
        CATGCTAAGTGCTACCCAGGGTGCAAATACCTATTGGATGAGAAGGGGCAAGAATATATA
   1081 ---------+---------+---------+---------+---------+---------+ 1140

a       H  A  K  C  Y  P  G  C  K  Y  L  L  D  E  K  G  Q  E  Y  I   -

        AATAATATTCATTTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAAACA
   1141 ---------+---------+---------+---------+---------+---------+ 1200

a       N  N  I  H  L  T  H  P  L  E  E  S  L  G  R  T  A  E  K  T   -

        CCACCGCTAACTAAAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAGAAGCT
   1201 ---------+---------+---------+---------+---------+---------+ 1260

a       P  P  L  T  K  K  I  D  D  T  I  F  Q  N  P  M  V  Q  E  A   -

        ATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAACAATGGAAGAAAAAATCCAAACA
   1261 ---------+---------+---------+---------+---------+---------+ 1320

a       I  R  M  G  F  S  F  K  D  L  K  K  T  M  E  E  K  I  Q  T   -

        TCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTCAGAAA
   1321 ---------+---------+---------+---------+---------+---------+ 1380

a       S  G  S  S  Y  L  S  L  E  V  L  I  A  D  L  V  S  A  Q  K   -

        GATAATACGGAGGATGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG
   1381 ---------+---------+---------+---------+---------+---------+ 1440

a       D  N  T  E  D  E  S  S  Q  T  S  L  Q  K  D  I  S  T  E  E   -
```

FIG. 4 (PAGE 4 OF 6)

MOUSE xiap

```
          CAGCTAAGGCGCCTACAAGAGGAGAAGCTTTCCAAAATCTGTATGGATAGAAATATTGCT
     1441 ---------+---------+---------+---------+---------+---------+ 1500

a         Q  L  R  R  L  Q  E  E  K  L  S  K  I  C  M  D  R  N  I  A   -

          ATCGTTTTTTTTCCTTGTGGACATCTGGCCACTTGTAAACAGTGTGCAGAAGCAGTTGAC
     1501 ---------+---------+---------+---------+---------+---------+ 1560

a         I  V  F  F  P  C  G  H  L  A  T  C  K  Q  C  A  E  A  V  D   -

          AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAAATTTTTATGTCTTAGTGG
     1561 ---------+---------+---------+---------+---------+---------+ 1620

a         K  C  P  M  C  Y  T  V  I  T  F  N  Q  K  I  F  M  S  *      -

          GGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGGAGCGAACTTTAAG
     1621 ---------+---------+---------+---------+---------+---------+ 1680

a                                                                      -

          TAATCCTGCATTTGCATTCCATTAGCATCCTGCTGTTTCCAAATGGAGACCAATGCTAAC
     1681 ---------+---------+---------+---------+---------+---------+ 1740

a                                                                      -

          AGCACTGTTTCCGTCTAAACATTCAATTTCTGGATCTTTCGAGTTATCAGCTGTATCATT
     1741 ---------+---------+---------+---------+---------+---------+ 1800

a                                                                      -
```

FIG. 4 (PAGE 5 OF 6)

MOUSE xiap

```
     TAGCCAGTGTTTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT
1801 ---------+---------+---------+---------+---------+---------+ 1860

a                                                                  -

     GTATATTGGTAGTACACTGACTTGATTTCTATATGTAAGTGAATTCATCACCTGCATGTT
1861 ---------+---------+---------+---------+---------+---------+ 1920

a                                                                  -

     TCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATGTGATG
1921 ---------+---------+---------+---------+---------+---------+ 1980

a                                                                  -

     GAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCCACGCTG
1981 ---------+---------+---------+---------+---------+---------+ 2040

a                                                                  -

     CTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATTCTGCCCATTTA
2041 ---------+---------+---------+---------+---------+---------+ 2100
```

FIG. 4 (PAGE 6 OF 6)

M-hiap-1

```
     GAATTCCGGGAGACCTACACCCCCGGAGATCAGAGGTCATTGCTGGCGTTCAGAGCCTAG
  1  ---------+---------+---------+---------+---------+---------+  60
     GAAGTGGGCTGCGGTATCAGCCTAGCAGTAAAACCGACCAGAAGCCATGCACAAAACTAC
 61  ---------+---------+---------+---------+---------+---------+  120
     ATCCCCAGAGAAAGACTTGTCCCTTCCCCTCCCTGTCATCTCACCATGAACATGGTTCAA
121  ---------+---------+---------+---------+---------+---------+  180
                                                    M  N  M  V  Q   -

     GACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGCTGACACCTTTGAGTTGAAGTATGAC
181  ---------+---------+---------+---------+---------+---------+  240
     D  S  A  F  L  A  K  L  M  K  S  A  D  T  F  E  L  K  Y  D   -

     TTTTCCTGTGAGCTGTACCGATTGTCCACGTATTCAGCTTTTCCCAGGGGAGTTCCTGTG
241  ---------+---------+---------+---------+---------+---------+  300
     F  S  C  E  L  Y  R  L  S  T  Y  S  A  F  P  R  G  V  P  V   -

     TCAGAAAGGAGTCTGGCTCGTGCTGGCTTTTACTACACTGGTGCCAATGACAAGGTCAAG
301  ---------+---------+---------+---------+---------+---------+  360
     S  E  R  S  L  A  R  A  G  F  Y  Y  T  G  A  N  D  K  V  K   -

     TGCTTCTGCTGTGGCCTGATGCTAGACAACTGGAAACAAGGGGACAGTCCCATGGAGAAG
361  ---------+---------+---------+---------+---------+---------+  420
     C  F  C  C  G  L  M  L  D  N  W  K  Q  G  D  S  P  M  E  K   -
```

FIG. 5 (PAGE 1 OF 6)

M-hiap-1

```
    CACAGAAAGTTGTACCCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGTCTG
421 ---------+---------+---------+---------+---------+---------+ 480
    H  R  K  L  Y  P  S  C  N  F  V  Q  T  L  N  P  A  N  S  L  -

    GAAGCTAGTCCTCGGCCTTCTCTTCCTTCCACGGCGATGAGCACCATGCCTTTGAGCTTT
481 ---------+---------+---------+---------+---------+---------+ 540
    E  A  S  P  R  P  S  L  P  S  T  A  M  S  T  M  P  L  S  F  -

    GCAAGTTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCCTCAGACCCT
541 ---------+---------+---------+---------+---------+---------+ 600
    A  S  S  E  N  T  G  Y  F  S  G  S  Y  S  S  F  P  S  D  P  -

    GTGAACTTCCGAGCAAATCAAGATTGTCCTGCTTTGAGCACAAGTCCCTACCACTTTGCA
601 ---------+---------+---------+---------+---------+---------+ 660
    V  N  F  R  A  N  Q  D  C  P  A  L  S  T  S  P  Y  H  F  A  -

    ATGAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCCATTGTCTTTTCTGTCA
661 ---------+---------+---------+---------+---------+---------+ 720
    M  N  T  E  K  A  R  L  L  T  Y  E  T  W  P  L  S  F  L  S  -

    CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
721 ---------+---------+---------+---------+---------+---------+ 780
    P  A  K  L  A  K  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C  -
```

FIG. 5 (PAGE 2 OF 6)

M-hiap-1

```
     TTTGCGTGCGATGGGAAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC
 781 ---------+---------+---------+---------+---------+---------+ 840
     F  A  C  D  G  K  L  S  N  W  E  R  K  D  D  A  M  S  E  H  -

     CAGAGGCATTTCCCCAGCTGTCCGTTCTTAAAAGACTTGGGTCAGTCTGCTTCGAGATAC
 841 ---------+---------+---------+---------+---------+---------+ 900
     Q  R  H  F  P  S  C  P  F  L  K  D  L  G  Q  S  A  S  R  Y  -

     ACTGTCTCTAACCTGAGCATGCAGACACACGCAGCCCGTATTAGAACATTCTCTAACTGG
 901 ---------+---------+---------+---------+---------+---------+ 960
     T  V  S  N  L  S  M  Q  T  H  A  A  R  I  R  T  F  S  N  W  -

     CCTTCTAGTGCACTAGTTCATTCCCAGGAACTTGCAAGTGCGGGCTTTTATTATACAGGA
 961 ---------+---------+---------+---------+---------+---------+ 1020
     P  S  S  A  L  V  H  S  Q  E  L  A  S  A  G  F  Y  Y  T  G  -

     CACAGTGATGATGTCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA
1021 ---------+---------+---------+---------+---------+---------+ 1080
     H  S  D  D  V  K  C  L  C  C  D  G  G  L  R  C  W  E  S  G  -

     GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTGCTCAGAATC
1081 ---------+---------+---------+---------+---------+---------+ 1140
     D  D  P  W  V  E  H  A  K  W  F  P  R  C  E  Y  L  L  R  I  -

     AAAGGCCAAGAATTTGTCAGCCAAGTTCAAGCTGGCTATCCTCATCTACTTGAGCAGCTA
1141 ---------+---------+---------+---------+---------+---------+ 1200
     K  G  Q  E  F  V  S  Q  V  Q  A  G  Y  P  H  L  L  E  Q  L  -
```

FIG. 5 (PAGE 3 OF 6)

M-hiap-1

```
     TTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCATTTTGGC
1201 ---------+---------+---------+---------+---------+---------+ 1260
     L  S  T  S  D  S  P  E  D  E  N  A  D  A  A  I  V  H  F  G   -

     CCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTTG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     P  G  E  S  S  E  D  V  V  M  M  S  T  P  V  V  K  A  A  L   -

     GAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT
1321 ---------+---------+---------+---------+---------+---------+ 1380
     E  M  G  F  S  R  S  L  V  R  Q  T  V  Q  W  Q  I  L  A  T   -

     GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     G  E  N  Y  R  T  V  S  D  L  V  I  G  L  L  D  A  E  D  E   -

     ATGAGAGAGGAGCAGATGGAGCAGGCGGCCGAGGAGGAGGAGTCAGATGATCTAGCACTA
1441 ---------+---------+---------+---------+---------+---------+ 1500
     M  R  E  E  Q  M  E  Q  A  A  E  E  E  E  S  D  D  L  A  L   -

     ATCCGGAAGAACAAAATGGTGCTTTTCCAACATTTGACGTGTGTGACACCAATGCTGTAT
1501 ---------+---------+---------+---------+---------+---------+ 1560
     I  R  K  N  K  M  V  L  F  Q  H  L  T  C  V  T  P  M  L  Y   -
```

FIG. 5 (PAGE 4 OF 6)

M-hiap-1

```
     TGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA
1561 ---------+---------+---------+---------+---------+---------+ 1620
     C  L  L  S  A  R  A  I  T  E  Q  E  C  N  A  V  K  Q  K  P   -

     CACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAAACACTGCAGCA
1621 ---------+---------+---------+---------+---------+---------+ 1680
     H  T  L  Q  A  S  T  L  I  D  T  V  L  A  K  G  N  T  A  A   -

     ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCTGCGTTATACAGAGATATATTTGTG
1681 ---------+---------+---------+---------+---------+---------+ 1740
     T  S  F  R  N  S  L  R  E  I  D  P  A  L  Y  R  D  I  F  V   -

     CAACAGGACATTAGGAGTCTTCCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG
1741 ---------+---------+---------+---------+---------+---------+ 1800
     Q  Q  D  I  R  S  L  P  T  D  D  I  A  A  L  P  M  E  E  Q   -

     TTGCGGCCCCTCCCGGAGGACAGAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC
1801 ---------+---------+---------+---------+---------+---------+ 1860
     L  R  P  L  P  E  D  R  M  C  K  V  C  M  D  R  E  V  S  I   -

     GTGTTCATTCCCTGTGGCCATCTGGTCGTGTGCAAAGACTGCGCTCCCTCTCTGAGGAAG
1861 ---------+---------+---------+---------+---------+---------+ 1920
     V  F  I  P  C  G  H  L  V  V  C  K  D  C  A  P  S  L  R  K   -
```

FIG. 5 (PAGE 5 OF 6)

M-hiap-1

```
     TGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGCGCACATTTCTCTCCTGAACAAGA
1921 ---------+---------+---------+---------+---------+---------+ 1980
     C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *         -

     CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCACTCCCAGTTCCAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACACACAAATATAAACAT
2041 ---------+---------+---------+---------+---------+---------+ 2100
     GAAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAATTTTAATTGGT
2101 ---------+---------+---------+---------+---------+---------+ 2160
     TTCCTTAAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTTCTGTAAACATATTTACA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATGAGAGAGGGTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TGTTCTTGTTCCTGAAAAGCTGGTTTATCATCTGATCAGCATATACTGCGCAACGGGCAG
2281 ---------+---------+---------+---------+---------+---------+ 2340
     GGCTAGAATCCATGAACCAAGCTGCAAAGATCTCACGCTAAATAAGGCGGAAAGATTTGG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     AGAAACGAAAGGAAATTCTTTCCTGTCCAATGTATACTCTTCAGACTAATGACCTCTTCC
2401 ---------+---------+---------+---------+---------+---------+ 2460
     TATCAAGCCTTCTA
2461 ---------+---- 2474
```

FIG. 5 (PAGE 6 OF 6)

M-hiap-2

```
     CTGTGGTGGAGATCTATTGTCCAAGTGGTGAGAAACTTCATCTGGAAGTTTAAGCGGTCA
   1 ---------+---------+---------+---------+---------+---------+ 60
     GAAATACTATTACTACTCATGGACAAAACTGTCTCCCAGAGACTCGCCCAAGGTACCTTA
  61 ---------+---------+---------+---------+---------+---------+ 120
     CACCCAAAAACTTAAACGTATAATGGAGAAGAGCACAATCTTGTCAAATTGGACAAAGGA
 121 ---------+---------+---------+---------+---------+---------+ 180
                            M  E  K  S  T  I  L  S  N  W  T  K  E  -

     GAGCGAAGAAAAAATGAAGTTTGACTTTTCGTGTGAACTCTACCGAATGTCTACATATTC
 181 ---------+---------+---------+---------+---------+---------+ 240
       S  E  E  K  M  K  F  D  F  S  C  E  L  Y  R  M  S  T  Y  S  -

     AGCTTTTCCCAGGGGAGTTCCTGTCTCAGAGAGGAGTCTGGCTCGTGCTGGCTTTTATTA
 241 ---------+---------+---------+---------+---------+---------+ 300
       A  F  P  R  G  V  P  V  S  E  R  S  L  A  R  A  G  F  Y  Y  -

     TACAGGTGTGAATGACAAAGTCAAGTGCTTCTGCTGTGGCCTGATGTTGGATAACTGGAA
 301 ---------+---------+---------+---------+---------+---------+ 360
       T  G  V  N  D  K  V  K  C  F  C  C  G  L  M  L  D  N  W  K  -

     ACAAGGGGACAGTCCTGTTGAAAAGCACAGACAGTTCTATCCCAGCTGCAGCTTTGTACA
 361 ---------+---------+---------+---------+---------+---------+ 420
       Q  G  D  S  P  V  E  K  H  R  Q  F  Y  P  S  C  S  F  V  Q  -
```

FIG. 6 (PAGE 1 OF 6)

M-hiap-2

```
    GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAATATGTCTCCTGTGAAAAGTAG
421 ---------+---------+---------+---------+---------+---------+ 480
     T  L  L  S  A  S  L  Q  S  P  S  K  N  M  S  P  V  K  S  R  -

    ATTTGCACATTCGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
481 ---------+---------+---------+---------+---------+---------+ 540
     F  A  H  S  S  P  L  E  R  G  G  I  H  S  N  L  C  S  S  P  -

    TCTTAATTCTAGAGCAGTGGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
541 ---------+---------+---------+---------+---------+---------+ 600
     L  N  S  R  A  V  E  D  F  S  S  R  M  D  P  C  S  Y  A  M  -

    GAGTACAGAAGAGGCCAGATTTCTTACTTACAGTATGTGGCCTTTAAGTTTTCTGTCACC
601 ---------+---------+---------+---------+---------+---------+ 660
     S  T  E  E  A  R  F  L  T  Y  S  M  W  P  L  S  F  L  S  P  -

    AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTTT
661 ---------+---------+---------+---------+---------+---------+ 720
     A  E  L  A  R  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C  F  -

    TGCCTGTGGTGGGAAACTGAGCAACTGGGAACCAAAGGATTATGCTATGTCAGAGCACCG
721 ---------+---------+---------+---------+---------+---------+ 780
     A  C  G  G  K  L  S  N  W  E  P  K  D  Y  A  M  S  E  H  R  -
```

FIG. 6 (PAGE 2 OF 6)

M-hiap-2

```
     CAGACATTTTCCCCACTGTCCATTTCTGGAAAATACTTCAGAAACACAGAGGTTTAGTAT
 781 ---------+---------+---------+---------+---------+---------+ 840
      R  H  F  P  H  C  P  F  L  E  N  T  S  E  T  Q  R  F  S  I  -

     ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC
 841 ---------+---------+---------+---------+---------+---------+ 900
      S  N  L  S  M  Q  T  H  S  A  R  L  R  T  F  L  Y  W  P  P  -

     TAGTGTTCCTGTTCAGCCCGAGCAGCTTGCAAGTGCTGGATTCTATTACGTGGATCGCAA
 901 ---------+---------+---------+---------+---------+---------+ 960
      S  V  P  V  Q  P  E  Q  L  A  S  A  G  F  Y  Y  V  D  R  N  -

     TGATGATGTCAAGTGCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA
 961 ---------+---------+---------+---------+---------+---------+ 1020
      D  D  V  K  C  L  C  C  D  G  G  L  R  C  W  E  P  G  D  D  -

     CCCCTGGATAGAACACGCCAAATGGTTTCCAAGGTGTGAGTTCTTGATACGGATGAAGGG
1021 ---------+---------+---------+---------+---------+---------+ 1080
      P  W  I  E  H  A  K  W  F  P  R  C  E  F  L  I  R  M  K  G  -

     TCAGGAGTTTGTTGATGAGATTCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTTGTC
1081 ---------+---------+---------+---------+---------+---------+ 1140
      Q  E  F  V  D  E  I  Q  A  R  Y  P  H  L  L  E  Q  L  L  S  -
```

FIG. 6 (PAGE 3 OF 6)

M-hiap-2

```
     CACTTCAGACACCCCAGGAGAAGAAAATGCTGACCCTACAGAGACAGTGGTGCATTTTGG
1141 ---------+---------+---------+---------+---------+---------+ 1200
      T  S  D  T  P  G  E  E  N  A  D  P  T  E  T  V  V  H  F  G  -

     CCCTGGAGAAAGTTCGAAAGATGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTT
1201 ---------+---------+---------+---------+---------+---------+ 1260
      P  G  E  S  S  K  D  V  V  M  M  S  T  P  V  V  K  A  A  L  -

     GGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCAC
1261 ---------+---------+---------+---------+---------+---------+ 1320
      E  M  G  F  S  R  S  L  V  R  Q  T  V  Q  R  Q  I  L  A  T  -

     TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA
1321 ---------+---------+---------+---------+---------+---------+ 1380
      G  E  N  Y  R  T  V  N  D  I  V  S  V  L  L  N  A  E  D  E  -

     GAGAAGAGAAGAGGAGAAGGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
1381 ---------+---------+---------+---------+---------+---------+ 1440
      R  R  E  E  E  K  E  R  Q  T  E  E  M  A  S  G  D  L  S  L  -

     GATTCGGAAGAATAGAATGGCCCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGA
1441 ---------+---------+---------+---------+---------+---------+ 1500
      I  R  K  N  R  M  A  L  F  Q  Q  L  T  H  V  L  P  I  L  D  -
```

FIG. 6 (PAGE 4 OF 6)

M-hiap-2

```
     TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAAC
1501 ---------+---------+---------+---------+---------+---------+ 1560
      N  L  L  E  A  S  V  I  T  K  Q  E  H  D  I  I  R  Q  K  T  -

     ACAGATACCCTTACAAGCAAGAGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGC
1561 ---------+---------+---------+---------+---------+---------+ 1620
      Q  I  P  L  Q  A  R  E  L  I  D  T  V  L  V  K  G  N  A  A  -

     AGCCAACATCTTCAAAAACTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACTTATT
1621 ---------+---------+---------+---------+---------+---------+ 1680
      A  N  I  F  K  N  S  L  K  G  I  D  S  T  L  Y  E  N  L  F  -

     TGTGGAAAAGAATATGAAGTATATTCCAACAGAAGACGTTTCAGGCTTGTCATTGGAAGA
1681 ---------+---------+---------+---------+---------+---------+ 1740
      V  E  K  N  M  K  Y  I  P  T  E  D  V  S  G  L  S  L  E  E  -

     GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTC
1741 ---------+---------+---------+---------+---------+---------+ 1800
      Q  L  R  R  L  Q  E  E  R  T  C  K  V  C  M  D  R  E  V  S  -

     TATTGTGTTCATTCCGTGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCCTTCTCTAAG
1801 ---------+---------+---------+---------+---------+---------+ 1860
      I  V  F  I  P  C  G  H  L  V  V  C  Q  E  C  A  P  S  L  R  -
```

FIG. 6 (PAGE 5 OF 6)

M-hiap-2

```
     GAAGTGCCCCATCTGCAGGGGACAATCAAGGGACTGTGCGCACATTTCTCTCATGAGT
1861 ---------+---------+---------+---------+---------+---------+ 1920
      K  C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *   -

     GAAGAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTAC
1921 ---------+---------+---------+---------+---------+---------+ 1980
     TGATTTCAGCTCTTCAGCAGGACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     GAAGGGTAGCATTGTATATTTAAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAG
2041 ---------+---------+---------+---------+---------+---------+ 2100
     CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA
2101 ---------+---------+---------+---------+---------+---------+ 2160
     CTTCTTGGGATTTGGGAATTTGGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TCCTGGAACCAGTGACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGGTAAAAATTTGCTGGATGTGAGAAAT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     AGATGAAAGTGTTTCGGGTGGGGGCGTGCATCAGTGTAGTGTGTGCAGGGATGTATGCAG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     GCCAAACACTGTGTAG
2401 ---------+------ 2416
```

FIG. 6 (PAGE 6 OF 6)

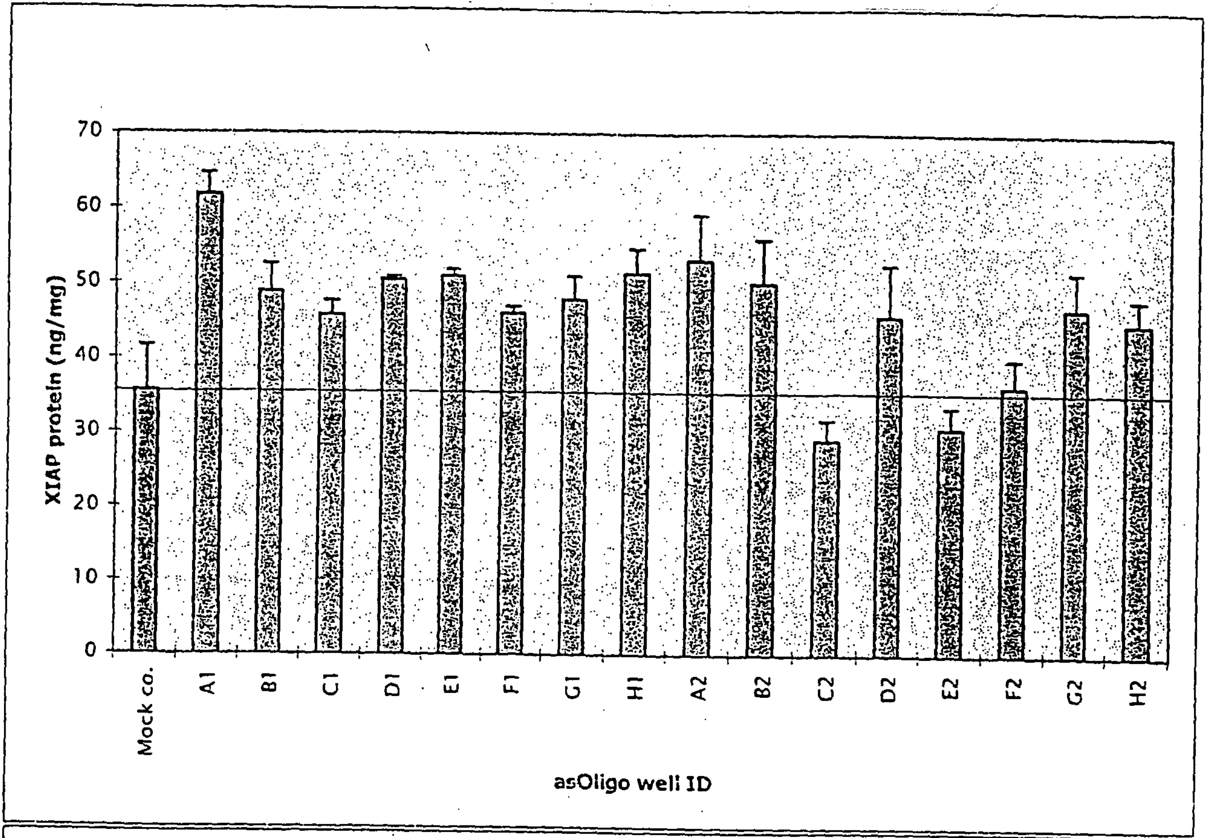

XIAP protein (ng/mg)
70
60
50
40
30
20
10
0
Mock co.
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
asOligo well ID

Fig. 7A

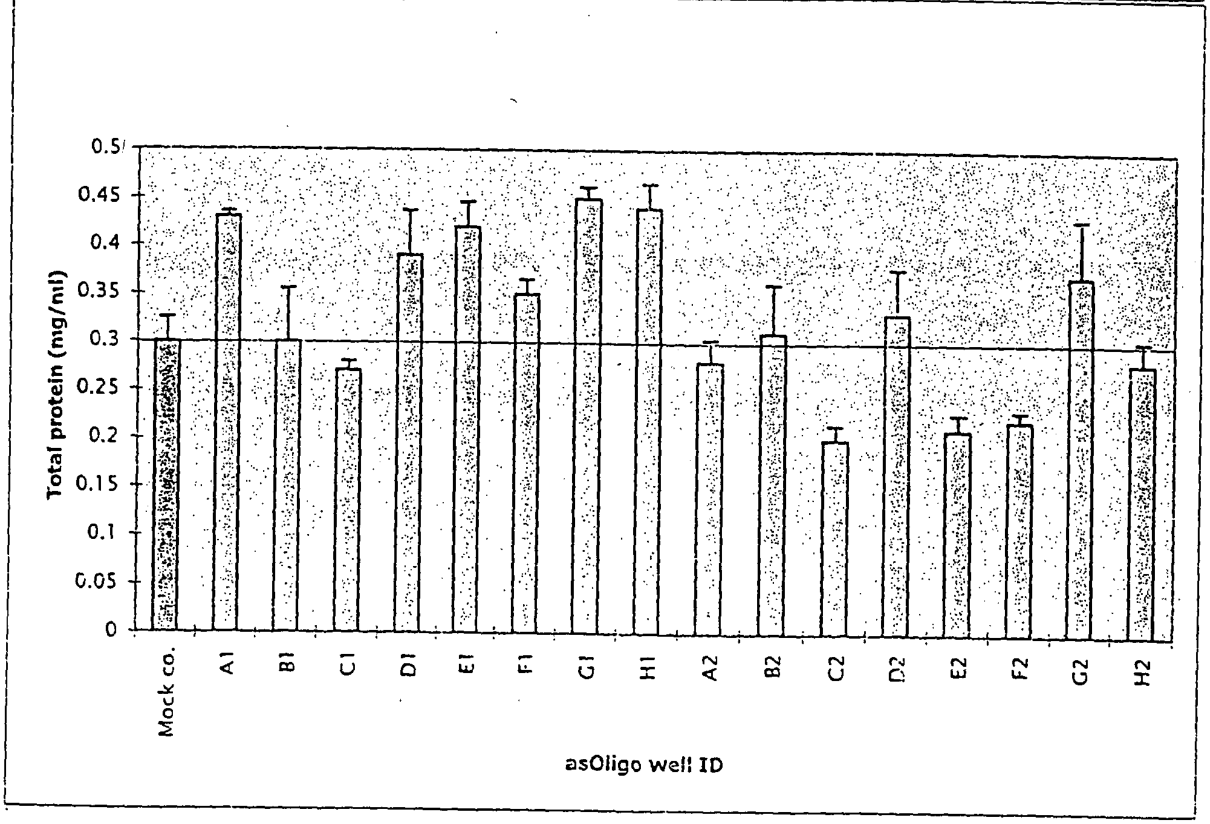

Total protein (mg/ml)
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Mock co.
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
asOligo well ID

Fig. 7B

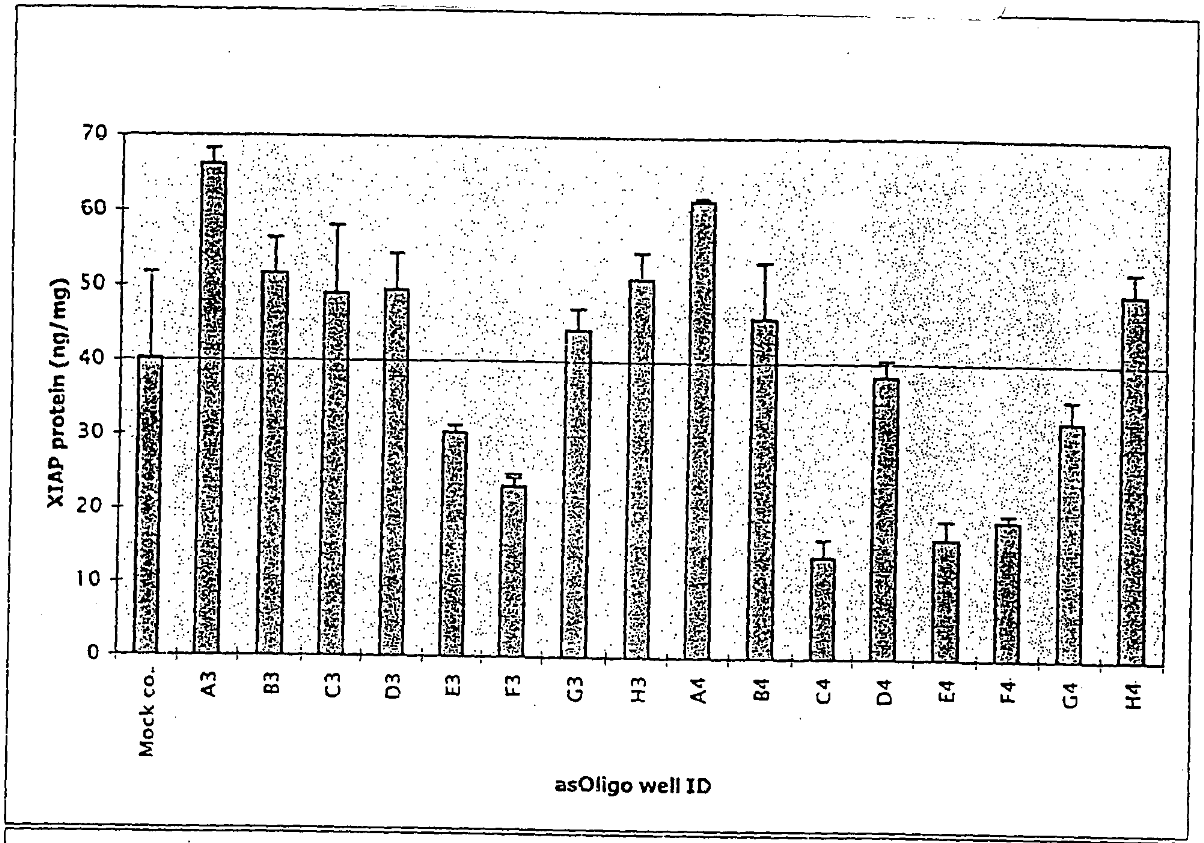

XIAP protein (ng/mg)
70
60
50
40
30
20
10
0
Mock co.
A3
B3
C3
D3
E3
F3
G3
H3
A4
B4
C4
D4
E4
F4
G4
H4
asOligo well ID

Fig. 7C

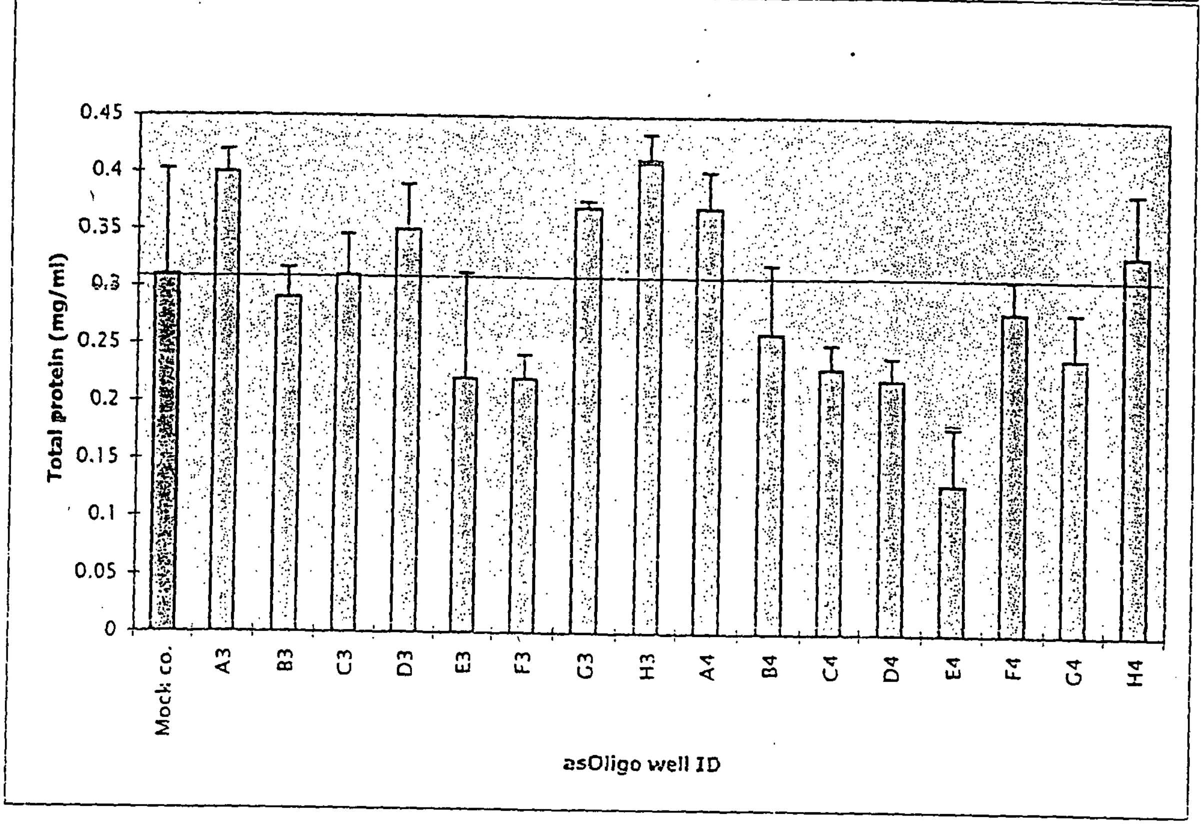

Total protein (mg/ml)
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Mock co.
A3
B3
C3
D3
E3
F3
G3
H3
A4
B4
C4
D4
E4
F4
G4
H4
asOligo well ID

Fig. 7D

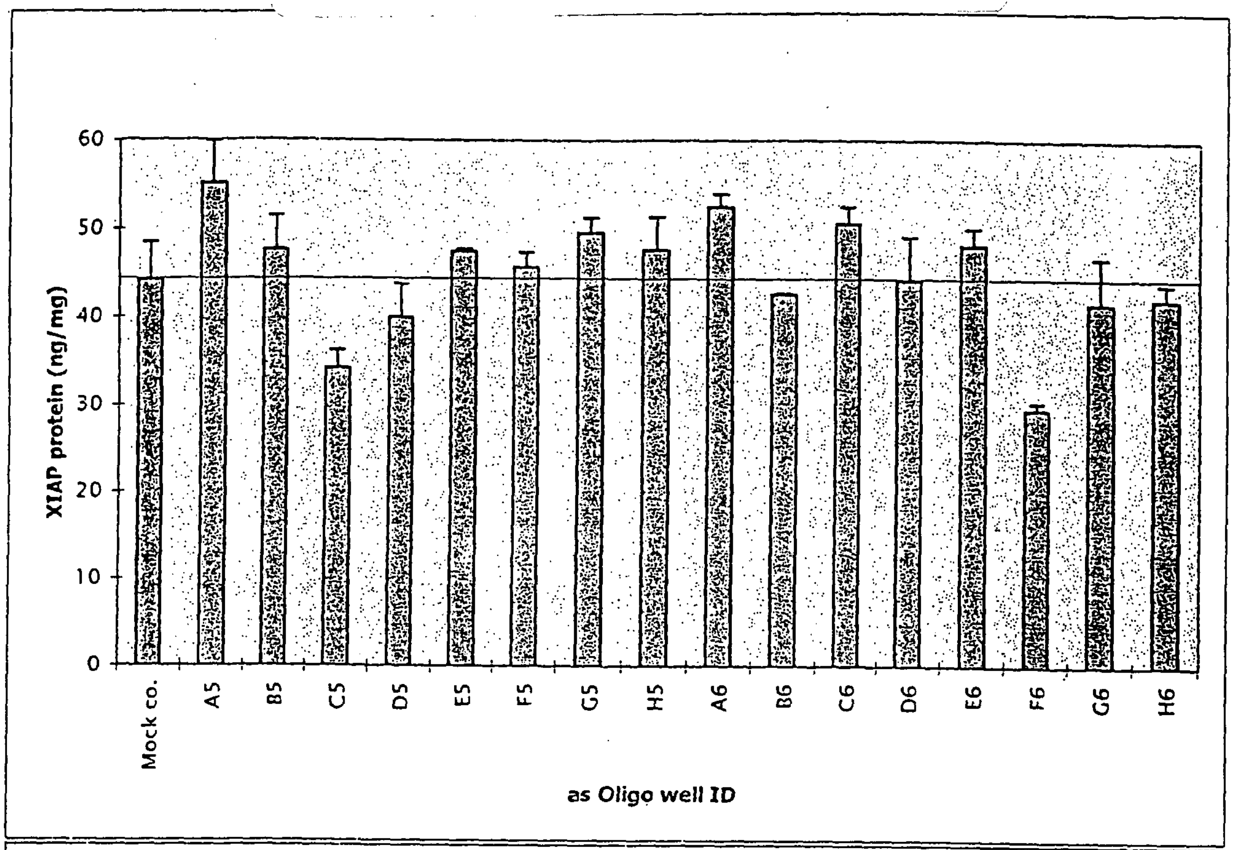

60
50
40
30
20
10
0
XIAP protein (ng/mg)
Mock co.
A5
B5
C5
D5
E5
F5
G5
H5
A6
B6
C6
D6
E6
F6
G6
H6
as Oligo well ID

Fig. 7E

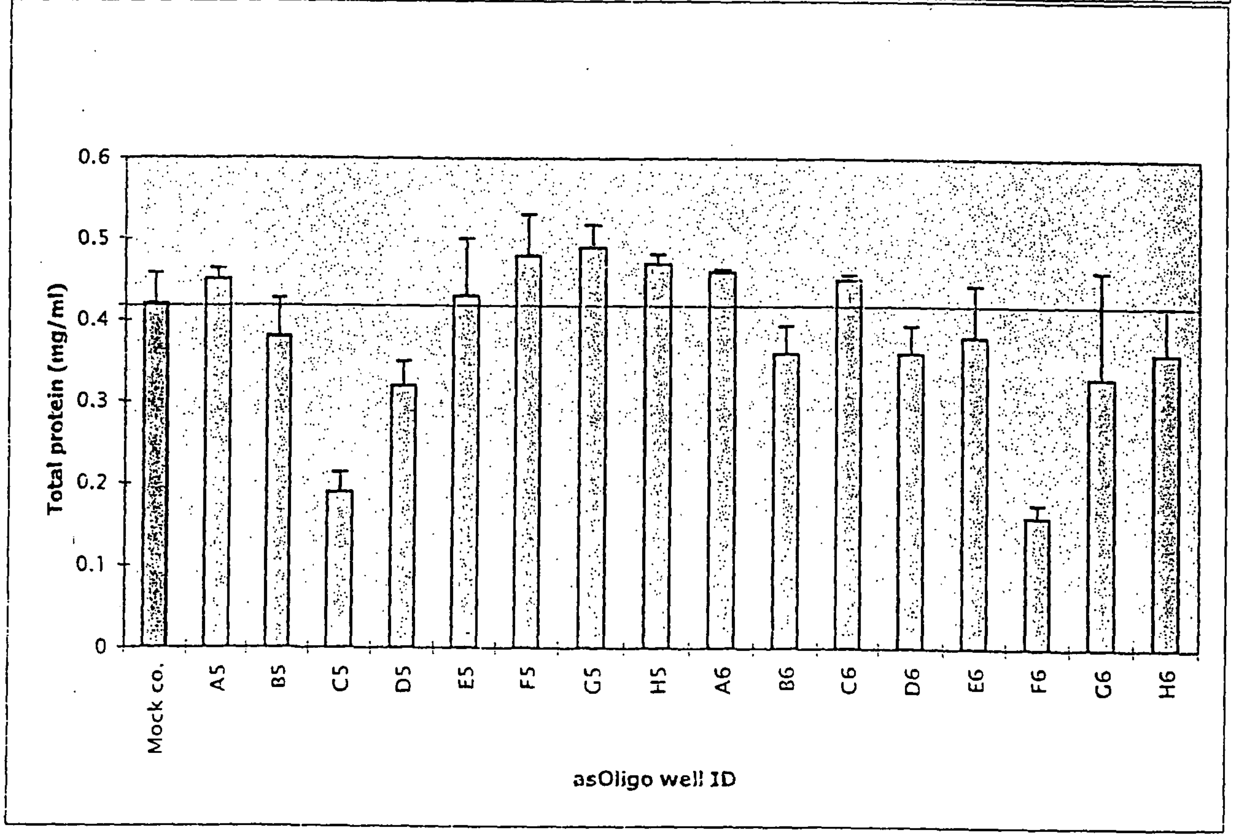

0.6
0.5
0.4
0.3
0.2
0.1
0
Total protein (mg/ml)
Mock co.
A5
B5
C5
D5
E5
F5
G5
H5
A6
B6
C6
D6
E6
F6
G6
H6
asOligo well ID

Fig. 7F

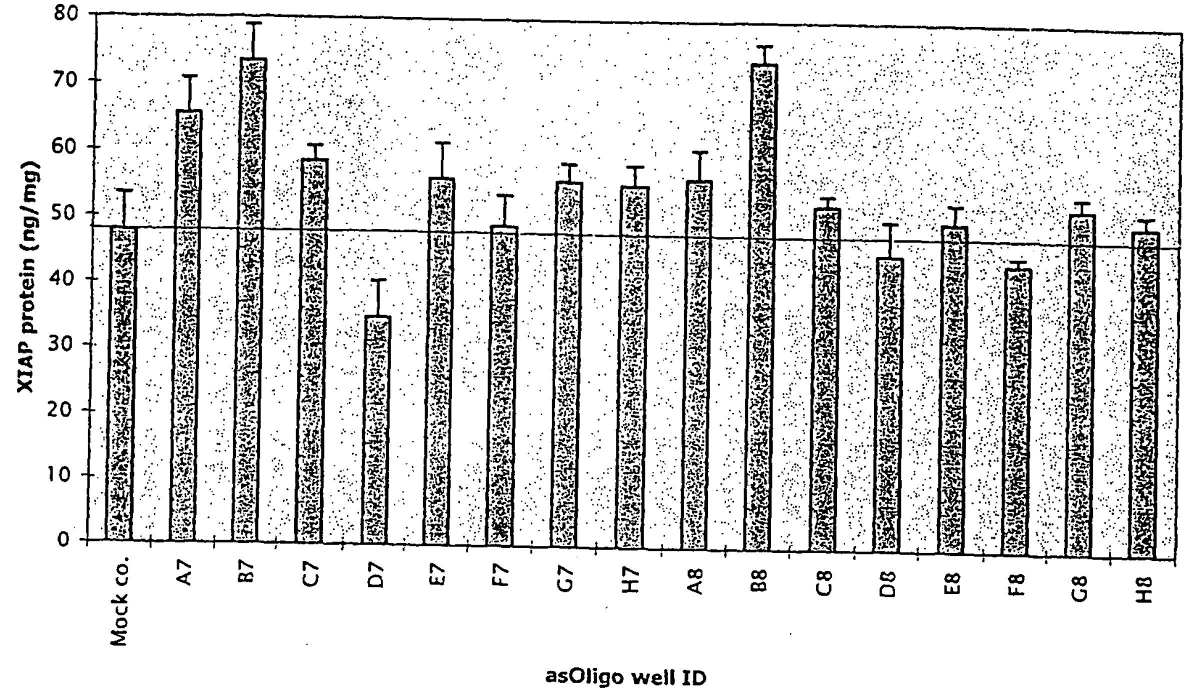

80
70
60
50
40
30
20
10
0
XIAP protein (ng/mg)
Mock co.
A7
B7
C7
D7
E7
F7
G7
H7
A8
B8
C8
D8
E8
F8
G8
H8
asOligo well ID

Fig. 7G

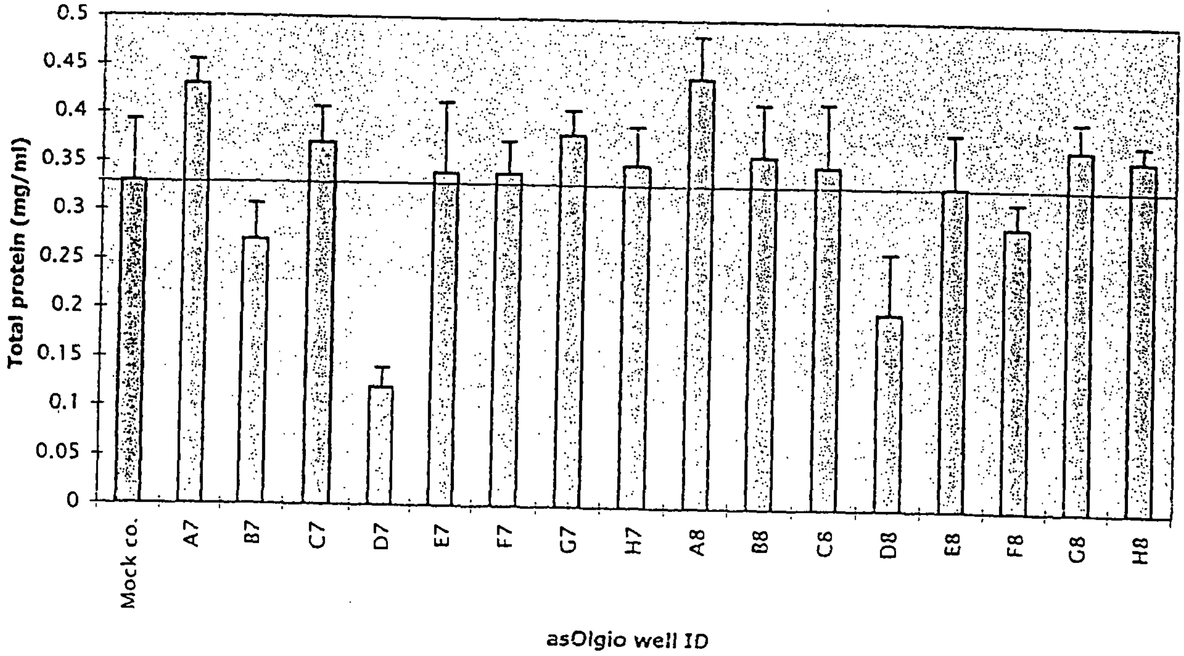

0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Total protein (mg/ml)
Mock co.
A7
B7
C7
D7
E7
F7
G7
H7
A8
B8
C8
D8
E8
F8
G8
H8
asOlgio well ID

Fig. 7H

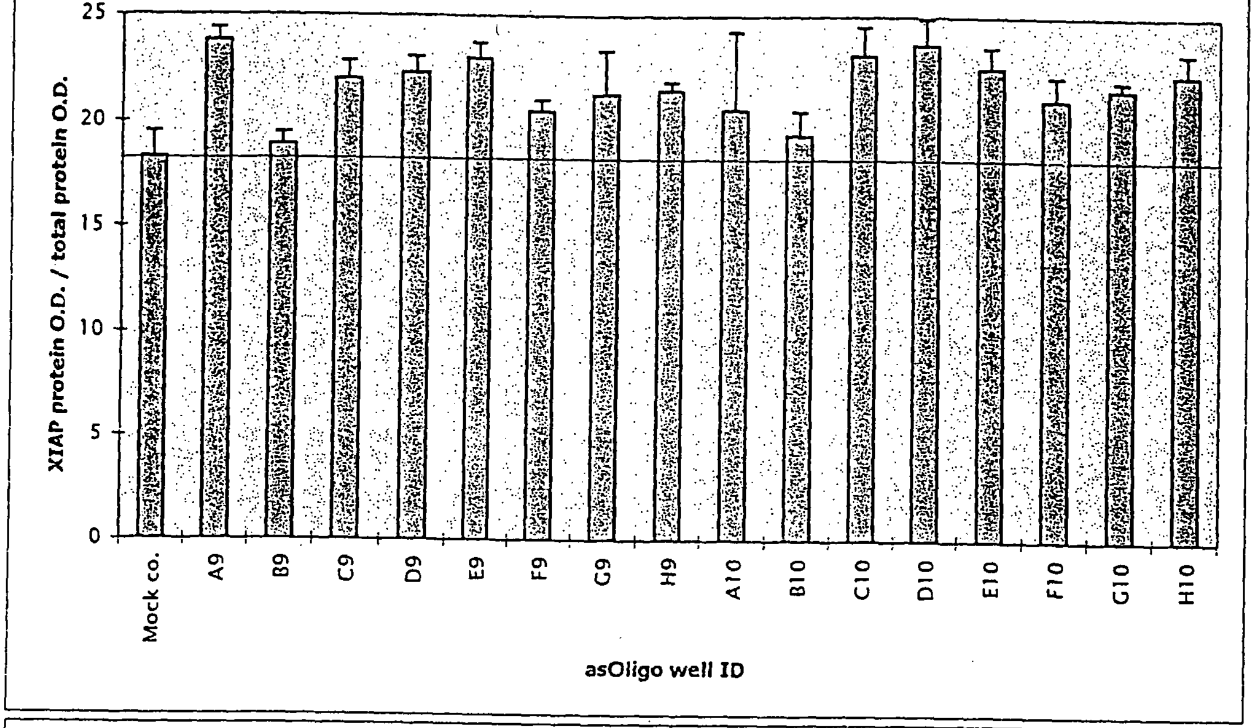

25
20
15
10
5
0
XIAP protein O.D. / total protein O.D.
Mock co.
A9
B9
C9
D9
E9
F9
G9
H9
A10
B10
C10
D10
E10
F10
G10
H10
asOligo well ID

Fig. 7I

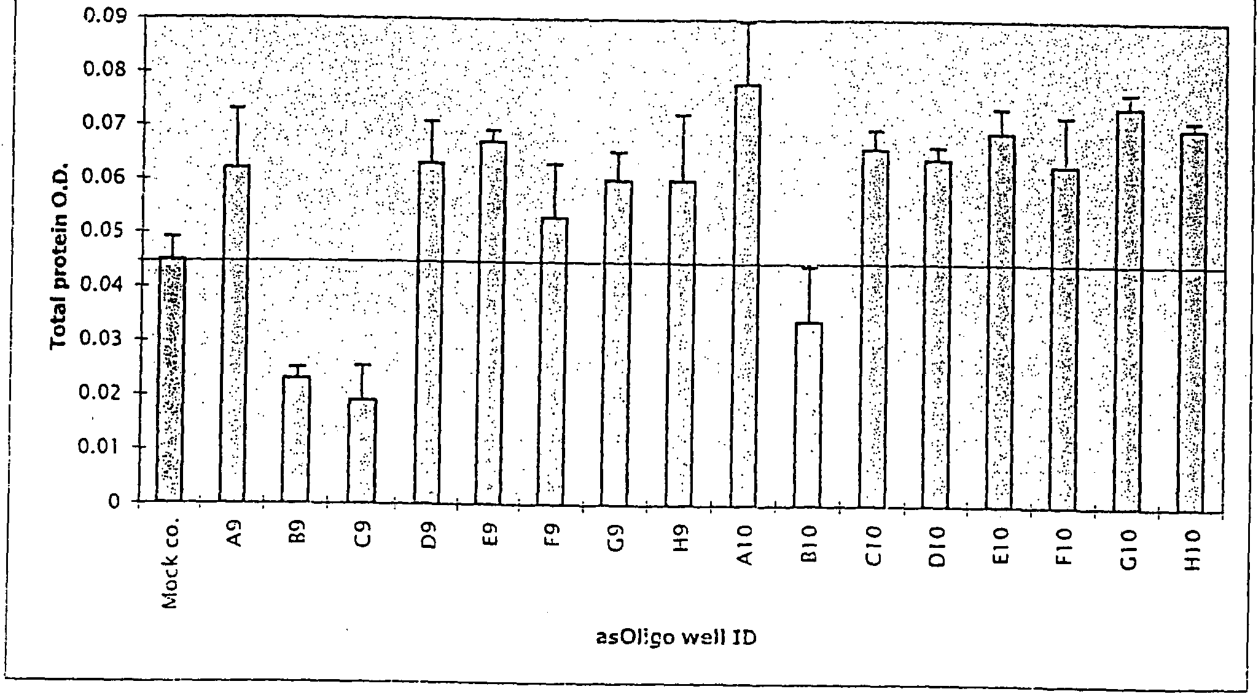

0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
Total protein O.D.
Mock co.
A9
B9
C9
D9
E9
F9
G9
H9
A10
B10
C10
D10
E10
F10
G10
H10
asOligo well ID

Fig. 7J

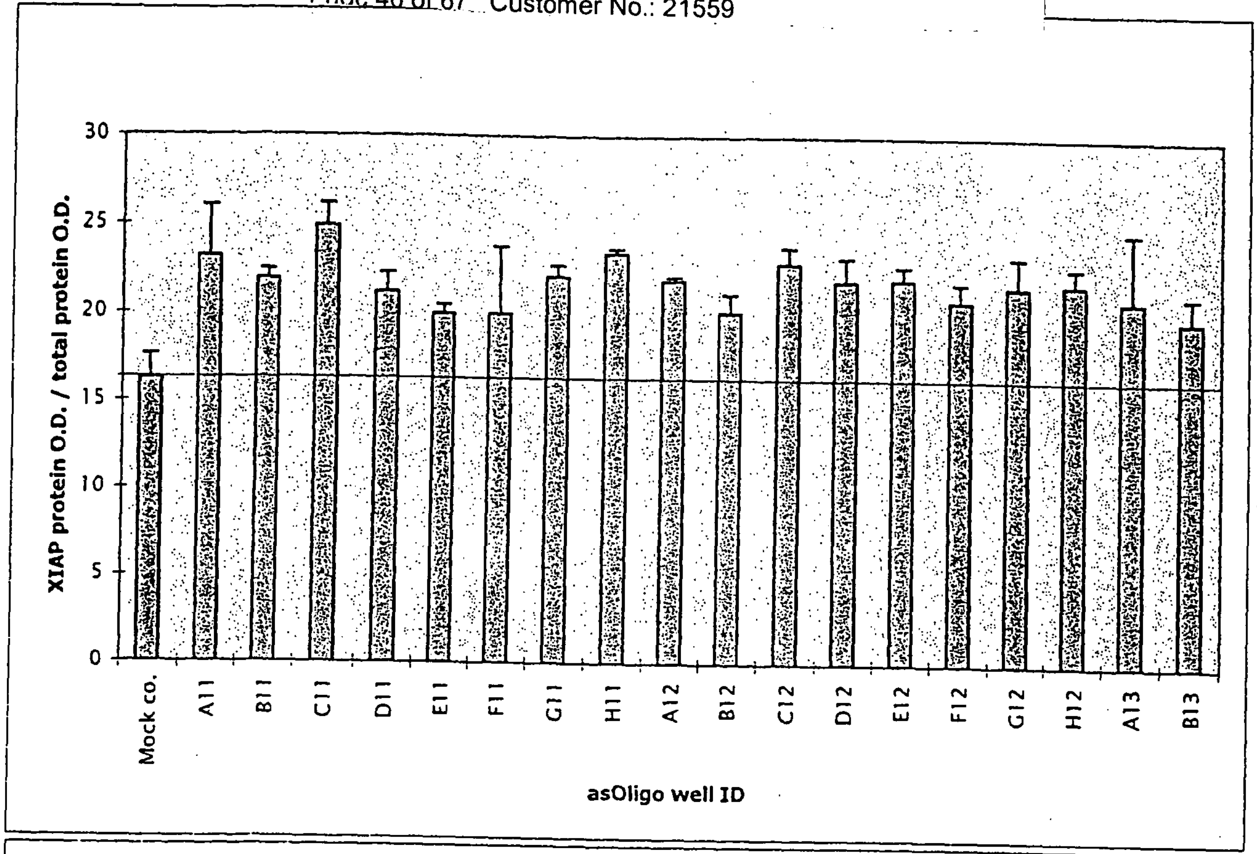

30
25
20
15
10
5
0
XIAP protein O.D. / total protein O.D.
Mock co.
A11
B11
C11
D11
E11
F11
G11
H11
A12
B12
C12
D12
E12
F12
G12
H12
A13
B13
asOligo well ID

Fig. 7K

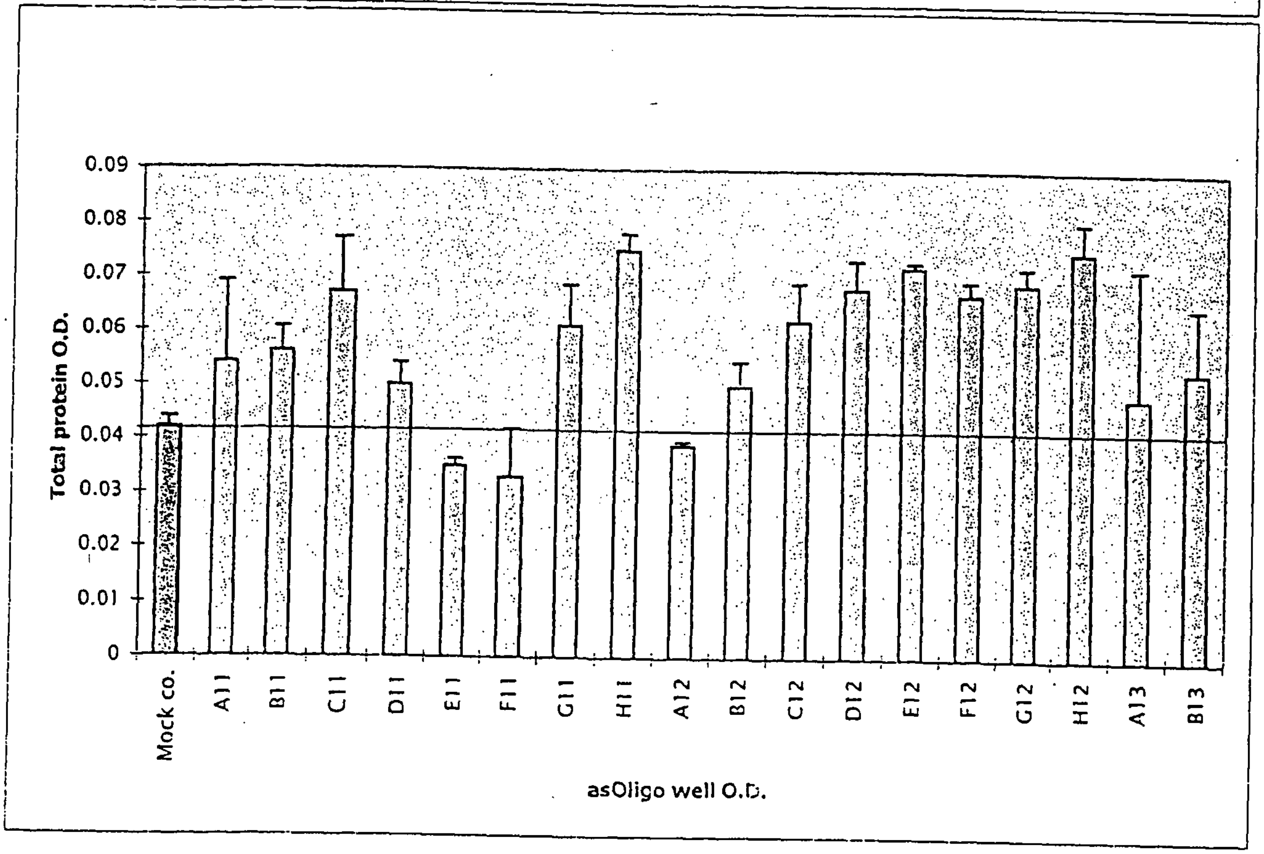

0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
Total protein O.D.
Mock co.
A11
B11
C11
D11
E11
F11
G11
H11
A12
B12
C12
D12
E12
F12
G12
H12
A13
B13
asOligo well O.D.

Fig. 7L

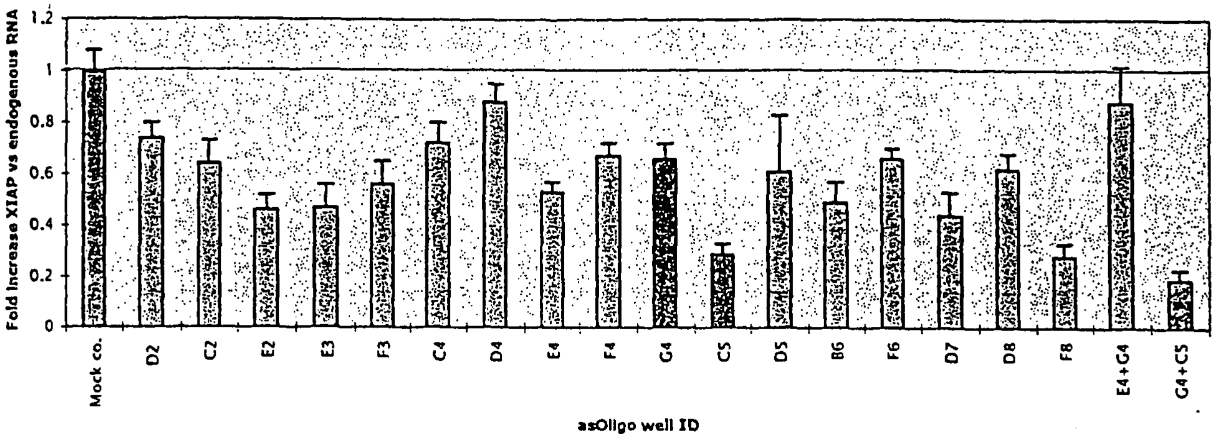


Fig. 8A

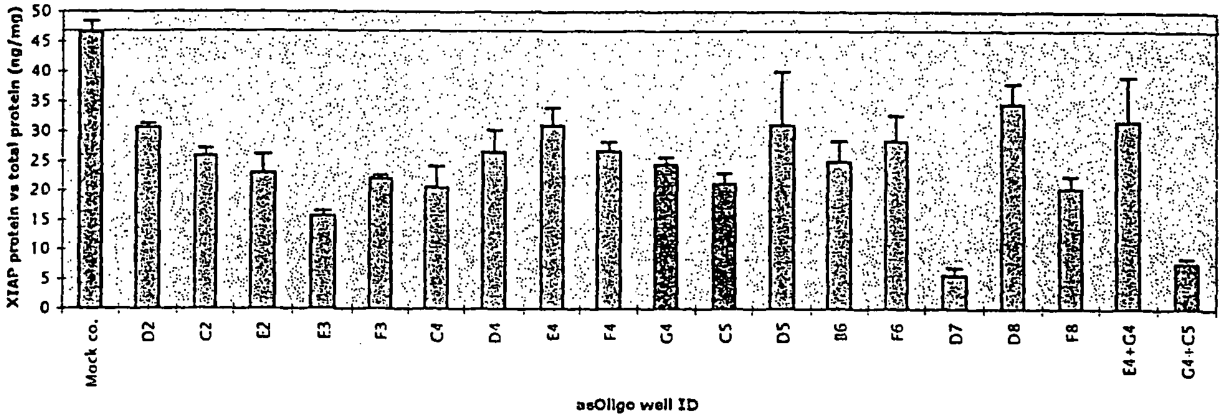


Fig. 8B

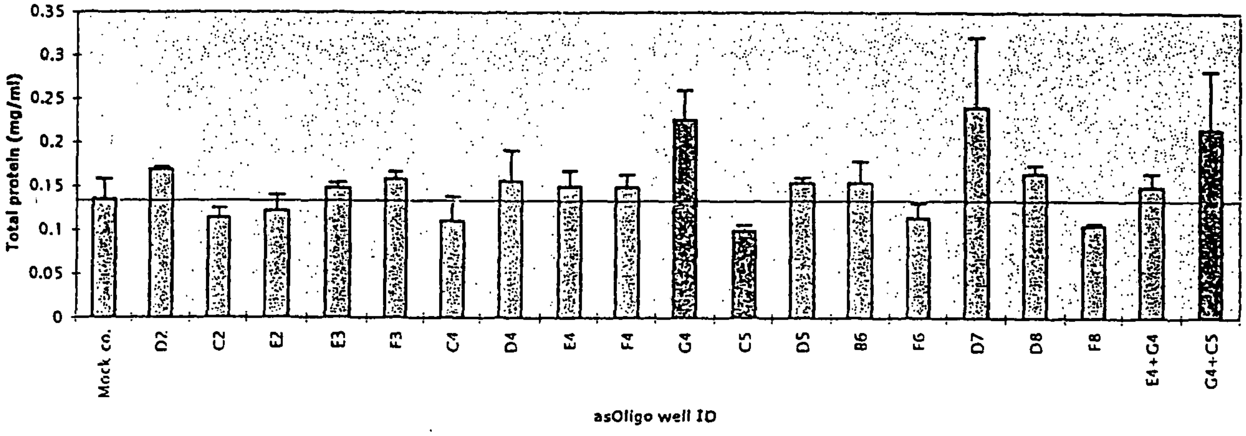


Fig. 8C

Title: ANTISENSE IAP OLIGONUCLEOTIDES AND USES THEREOF
Applicant(s): Robert G. Korneluk et al.
Filing Date: August 7, 2003 Serial No.:
Page 48 of 67 Customer No.: 21559

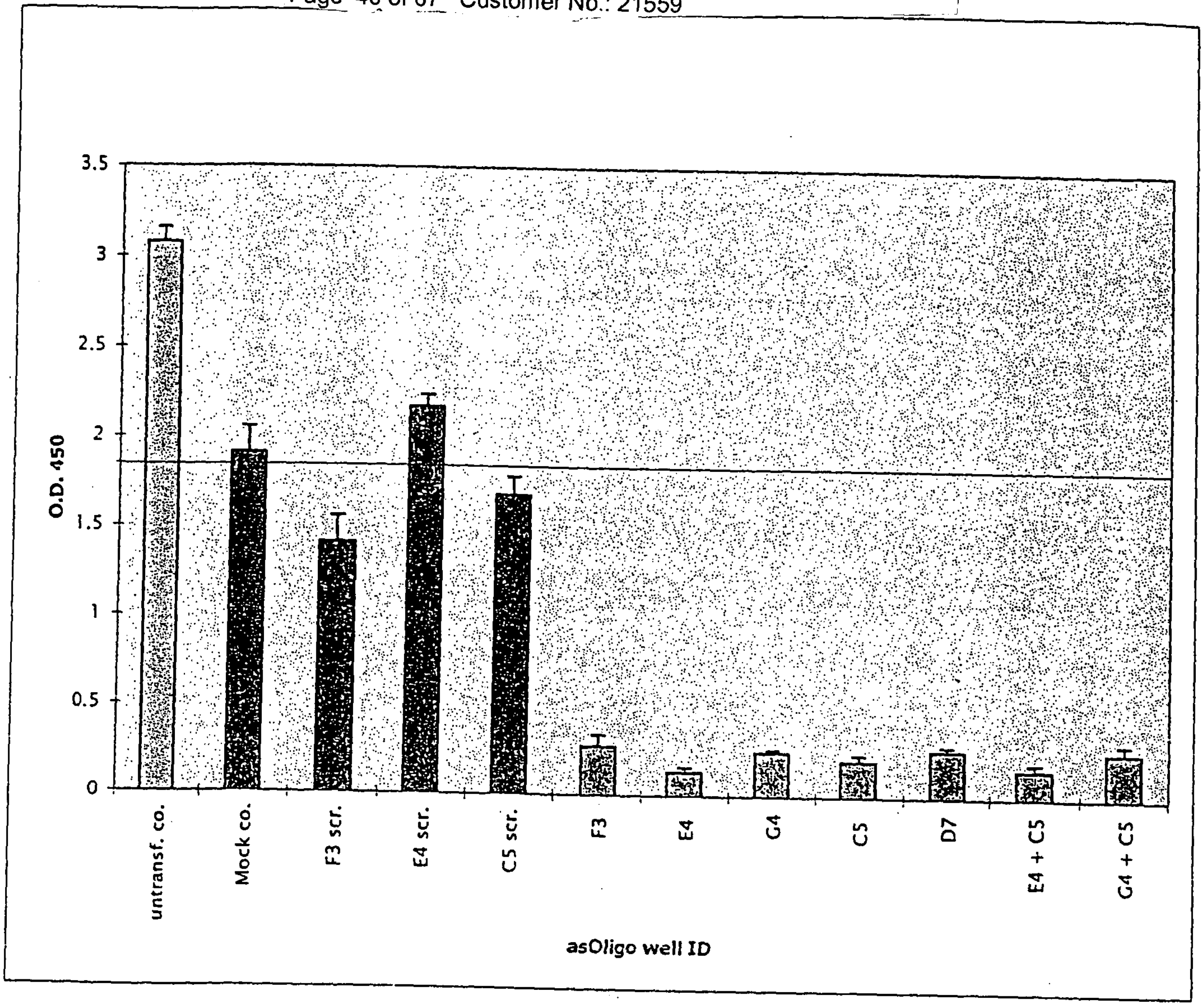


Fig. 9A

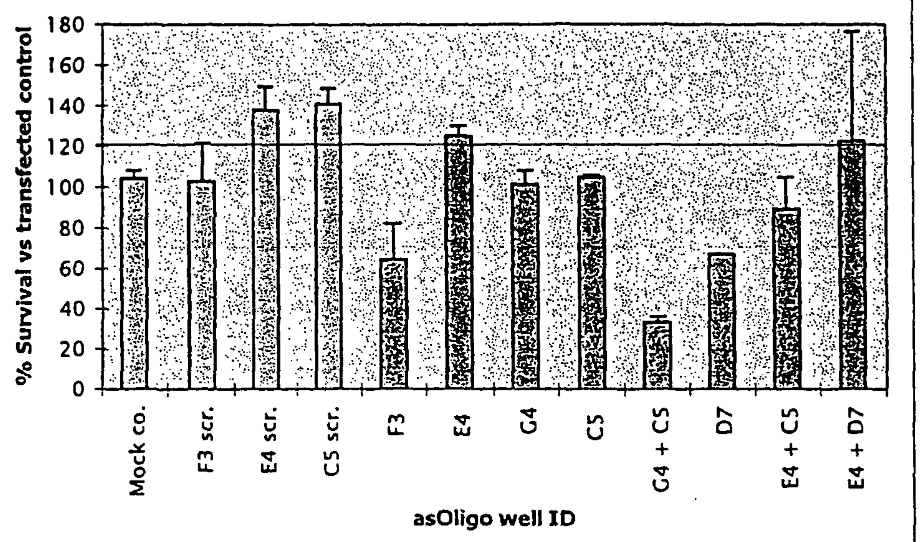

% Survival vs transfected control
180
160
140
120
100
80
60
40
20
0
Mock co.
F3 scr.
E4 scr.
C5 scr.
F3
E4
G4
C5
G4 + C5
D7
E4 + C5
E4 + D7
asOligo well ID

Fig. 9B

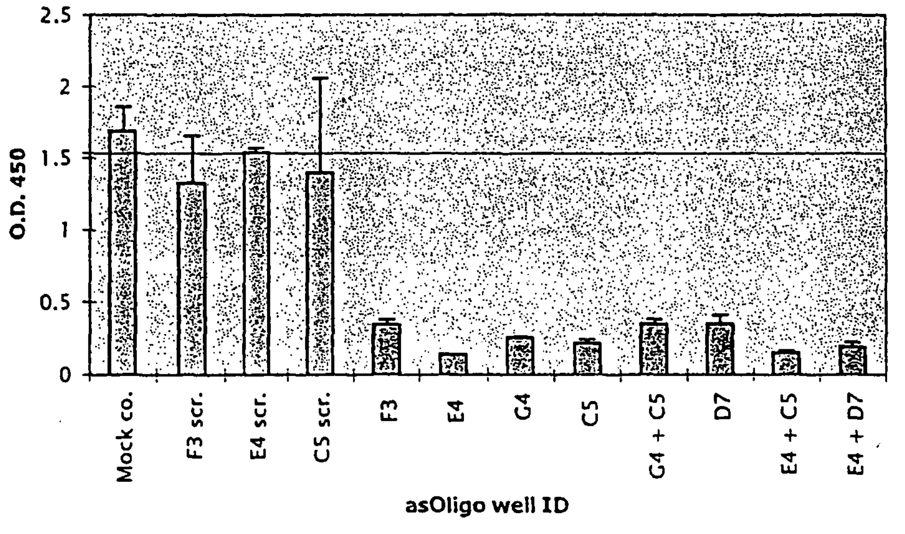
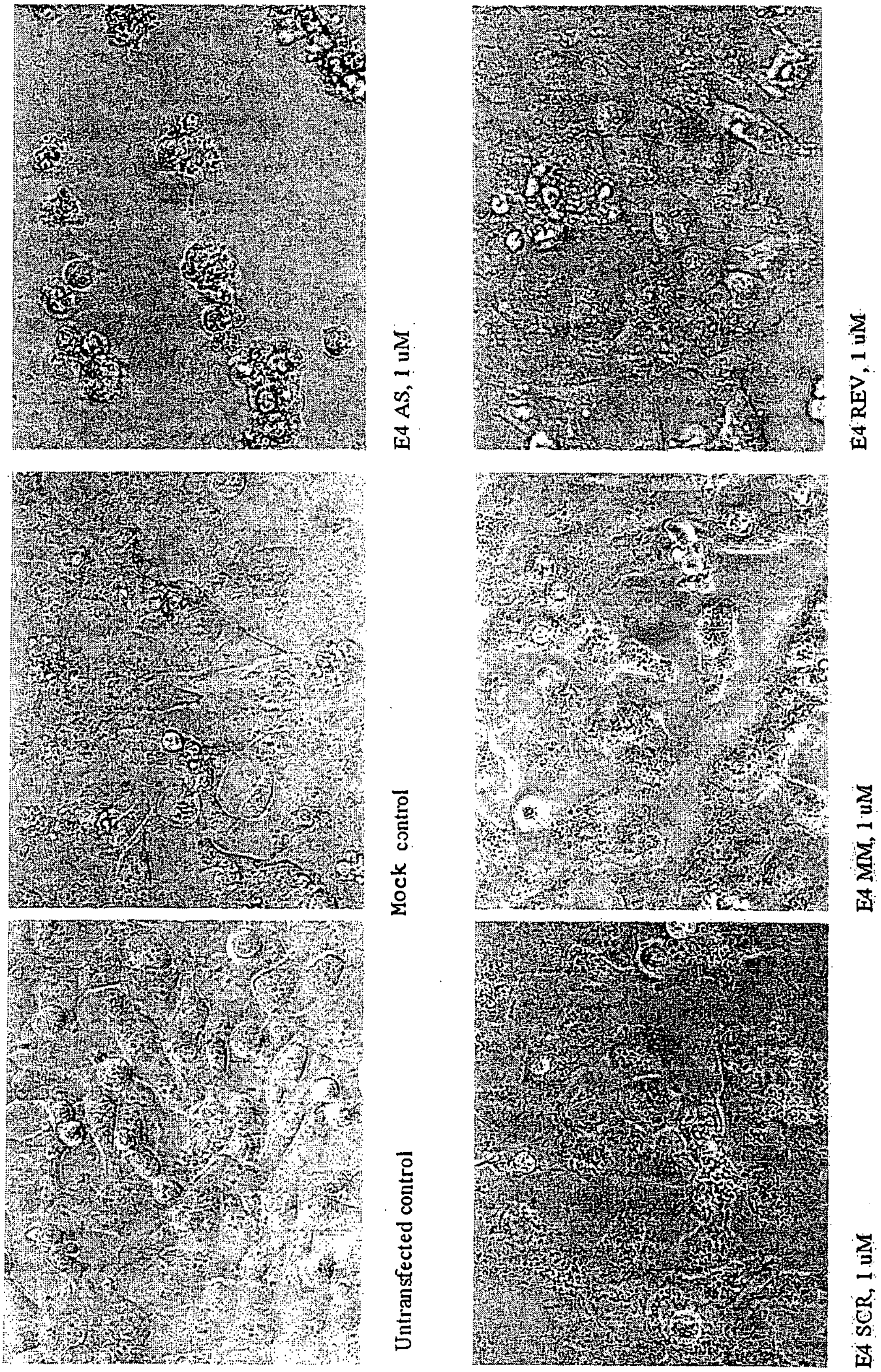

O.D. 450
2.5
2
1.5
1
0.5
0
Mock co.
F3 scr.
E4 scr.
C5 scr.
F3
E4
G4
C5
G4 + C5
D7
E4 + C5
E4 + D7
asOligo well ID

Fig. 9C


E4 AS, 1 uM

Mock control

Untransfected control

E4 REV, 1 uM

E4 MM, 1 uM

E4 SCR, 1 uM

Fig. 9D

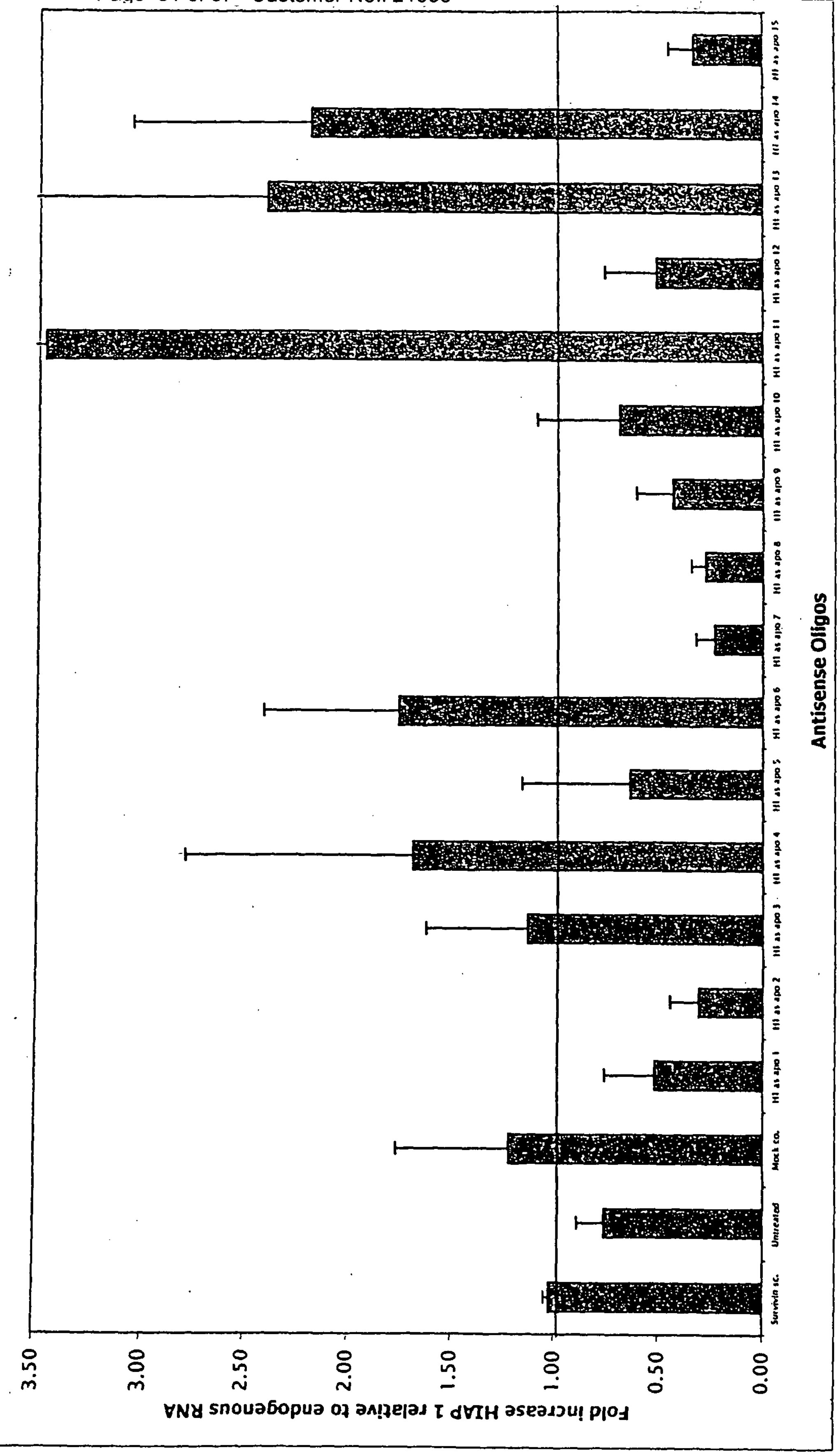

Fold increase HIAP 1 relative to endogenous RNA
3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
Survivin sc.
Untreated
Mock co.
H1 as apo 1
H1 as apo 2
H1 as apo 3
H1 as apo 4
H1 as apo 5
H1 as apo 6
H1 as apo 7
H1 as apo 8
H1 as apo 9
H1 as apo 10
H1 as apo 11
H1 as apo 12
H1 as apo 13
H1 as apo 14
H1 as apo 15
Antisense Oligos

Fig. 10

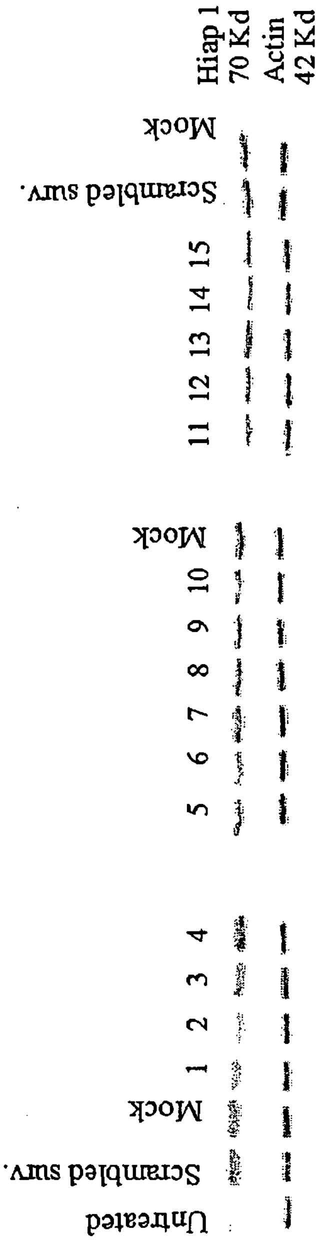


Fig. 11A

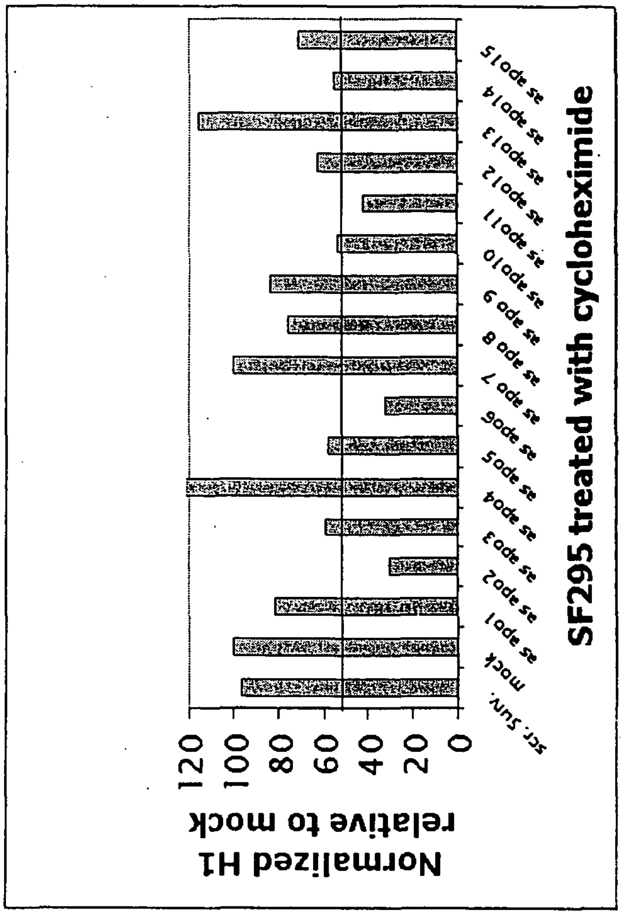


Fig. 11B

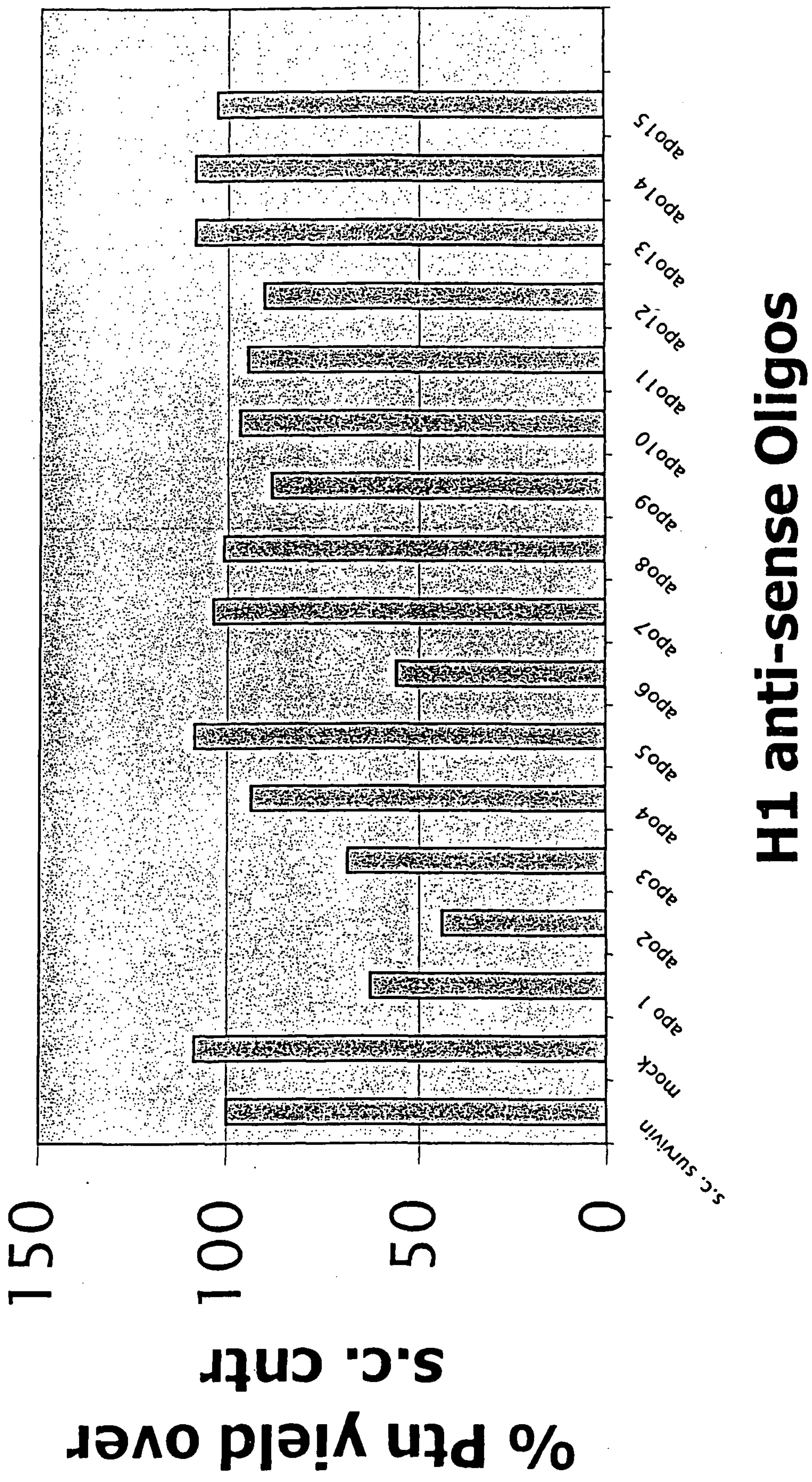

H1 anti-sense Oligos
% Ptn yield over s.c. cntr
150
100
50
0
s.c. survivin
mock
apo 1
apo2
apo3
apo4
apo5
apo6
apo7
apo8
apo9
apo10
apo11
apo12
apo13
apo14
apo15

Fig. 12

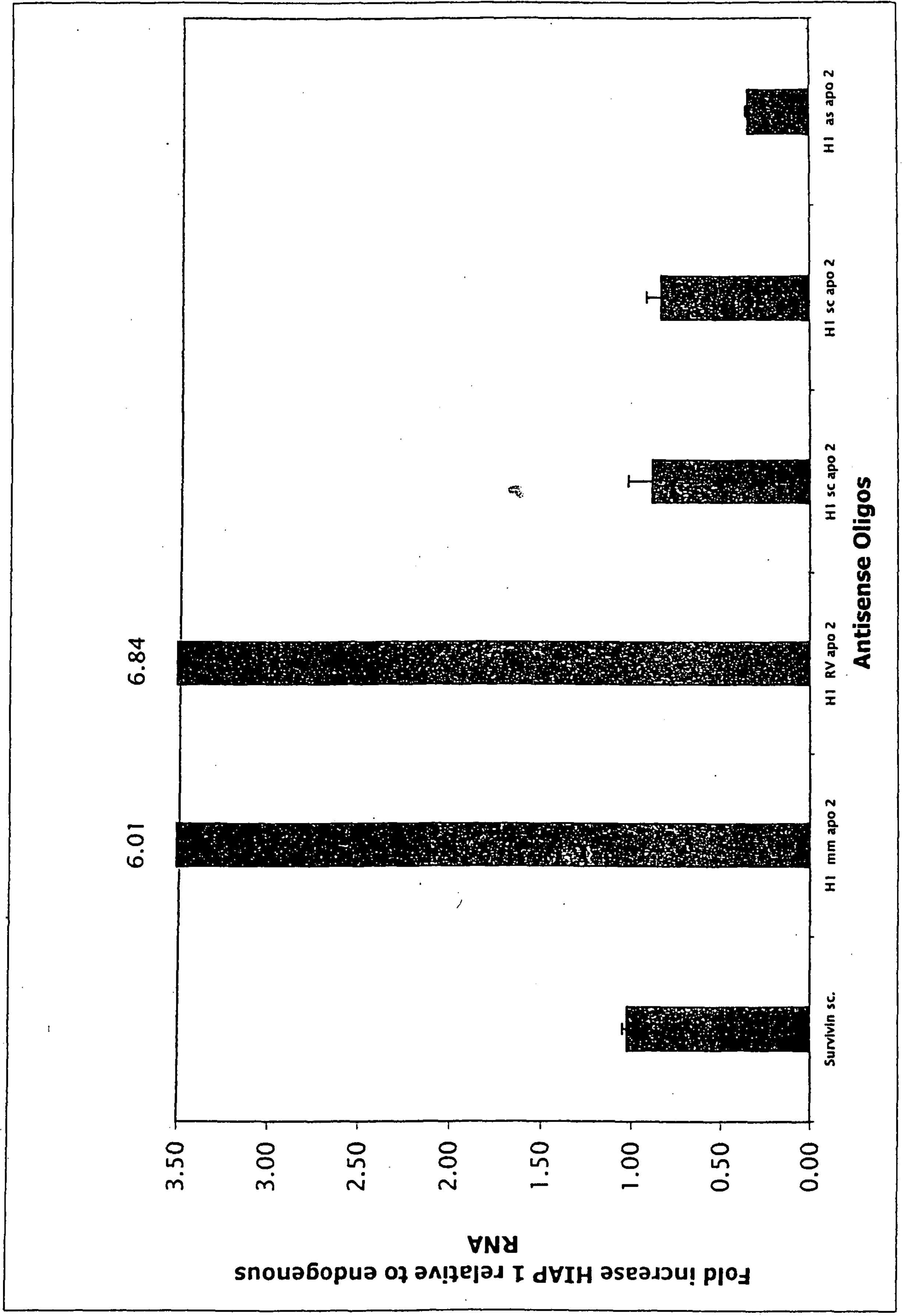

Fold increase HIAP 1 relative to endogenous RNA
3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
6.01
6.84
Survivin sc.
H1 mm apo 2
H1 RV apo 2
H1 sc apo 2
H1 sc apo 2
H1 as apo 2
Antisense Oligos

Fig. 13

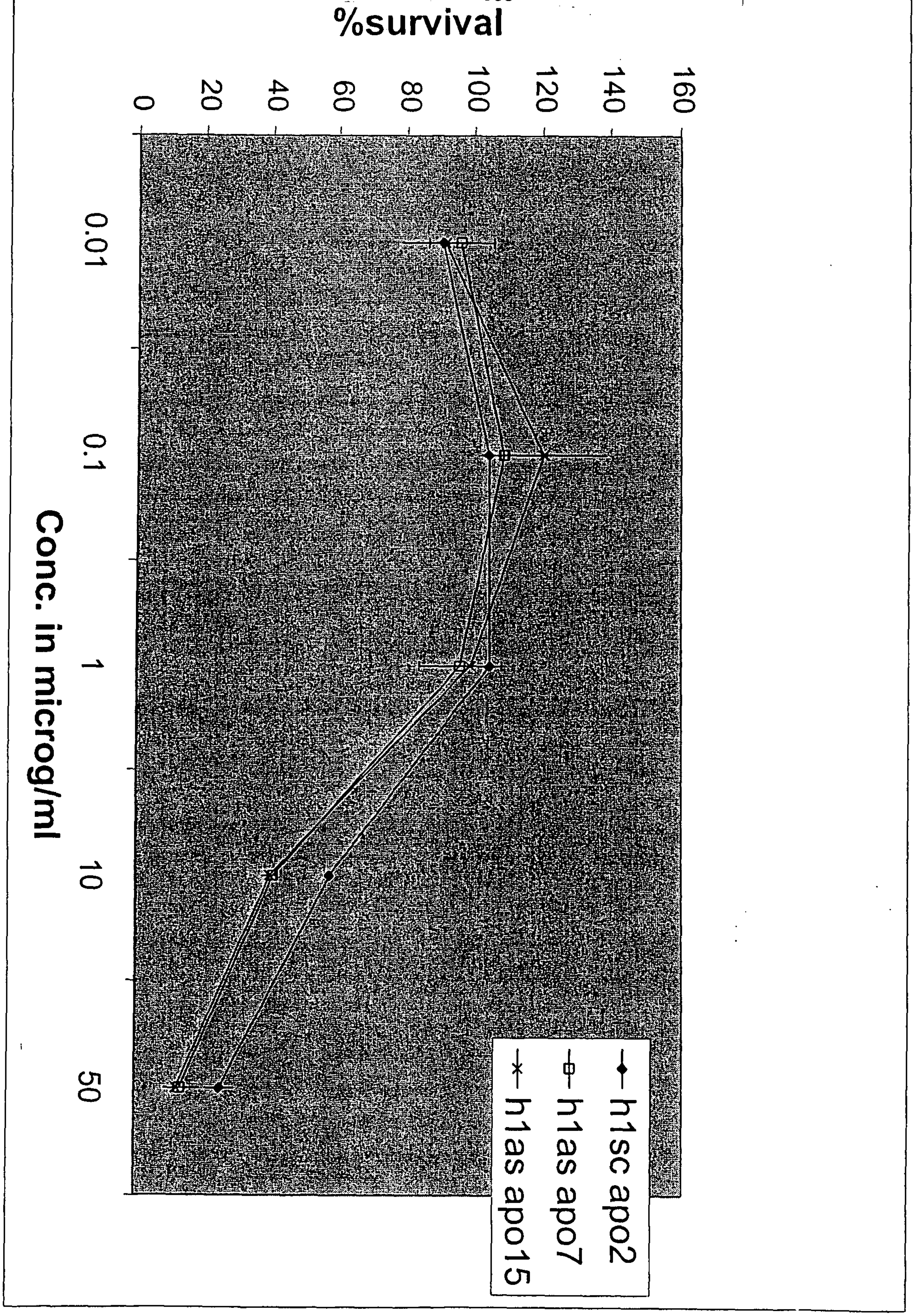

%survival
0
20
40
60
80
100
120
140
160
0.01
0.1
1
10
50
Conc. in microg/ml
h1sc apo2
h1as apo7
h1as apo15

Fig. 14

1 TTGCAGGTAC TTAGAATTTT TCCTGAGCCA CCCTCTAGAG GGCAGTGTTA
51 CATATATATC TGTAATTATC CAGTTACAAC AAAAAAAGGG CTCTCATTCA
101 TGCATGAAAA TCAGAAATAT TTCATACTCT TAAAGAACAC ATTGGAACCA
151 ATATTATGAT TAAAACATAT TTTGCTAAGC AAAGAGATAT TAAAAATTAA
201 TTCATTAACA TTCTGAACAT TTTTAACTT GTAAAAACAA CTTTGATGCC
251 TTGAATATAT AATGATTCAT TATAACAATT ATGCATAGAT TTTAATAATC
301 TGCATATTTT ATGCTTTCAT GTTTTCCTA ATTAATGATT TGACATGGTT
351 AATAATTATA ATATATTCTG CATCACAGTT TACATATTTA TGTAAAATAA
401 GCATTTAAAA ATTATTAGTT TTATTCTGCC TGCTTAAATA TTACTTTCCT
451 CAAAAAGAGA AAACAAAAAT GCTAGATTTT ACTTTATGAC TTGAATGATG
501 TGGTAATGTC GAACTCTAGT ATTTAGAATT AGAATGTTTC TTAGCGGTCG
551 TGTAGTTATT TTTATGTCAT AAGTGGATAA TTTGTTAGCT CCTATAACAA
601 AAGTCTGTTG CTTGTGTTTC ACATTTTGGA TTTCCTAATA TAATGTTCTC
651 TTTTTAGAAA AGGTGGACAA GTCCTATTTT CAAGAGAAGA TGACTTTTAA
701 CAGTTTTGAA GGATCTAAAA CTTGTGTACC TGCAGACATC AATAAGGAAG
751 AAGAATTTGT AGAAGAGTTT AATAGATTAA AAACTTTTGC TAATTTTCCA
801 AGTGGTAGTC CTGTTTCAGC ATCAACACTG GCACGAGCAG GGTTTCTTTA
851 TACTGGTGAA GGAGATACCG TGCGGTGCTT TAGTTGTCAT GCAGCTGTAG
901 ATAGATGGCA ATATGGAGAC TCAGCAGTTG GAAGACACAG GAAAGTATCC
951 CCAAATTGCA GATTTATCAA CGGCTTTTAT CTTGAAAATA GTGCCACGCA

Fig. 15 (Page 1 of 3)

1001 GTCTACAAAT TCTGGTATCC AGAATGGTCA GTACAAAGTT GAAAACTATC

1051 TGGGAAGCAG AGATCATTTT GCCTTAGACA GGCCATCTGA GACACATGCA

1101 GACTATCTTT TGAGAACTGG GCAGGTTGTA GATATATCAG ACACCATATA

1151 CCCGAGGAAC CCTGCCATGT ATTGTGAAGA AGCTAGATTA AAGTCCTTTC

1201 AGAACTGGCC AGACTATGCT CACCTAACCC CAAGAGAGTT AGCAAGTGCT

1251 GGACTCTACT ACACAGGTAT TGGTGACCAA GTGCAGTGCT TTTGTTGTGG

1301 TGGAAAACTG AAAAATTGGG AACCTTGTGA TCGTGCCTGG TCAGAACACA

1351 GGCGACACTT TCCTAATTGC TTCTTTGTTT TGGGCCGGAA TCTTAATATT

1401 CGAAGTGAAT CTGATGCTGT GAGTTCTGAT AGGAATTTCC CAAATTCAAC

1451 AAATCTTCCA AGAAATCCAT CCATGGCAGA TTATGAAGCA CGGATCTTTA

1501 CTTTTGGGAC ATGGATATAC TCAGTTAACA AGGAGCAGCT TGCAAGAGCT

1551 GGATTTTATG CTTTAGGTGA AGGTGATAAA GTAAAGTGCT TTCACTGTGG

1601 AGGAGGGCTA ACTGATTGGA AGCCCAGTGA AGACCCTTGG GAACAACATG

1651 CTAAATGGTA TCCAGGGTGC AAATATCTGT TAGAACAGAA GGGACAAGAA

1701 TATATAAACA ATATTCATTT AACTCATTCA CTTGAGGAGT GTCTGGTAAG

1751 AACTACTGAG AAAACACCAT CACTAACTAG AAGAATTGAT GATACCATCT

1801 TCCAAAATCC TATGGTACAA GAAGCTATAC GAATGGGGTT CAGTTTCAAG

1851 GACATTAAGA AAATAATGGA GGAAAAAATT CAGATATCTG GGAGCAACTA

1901 TAAATCACTT GAGGTTCTGG TTGCAGATCT AGTGAATGCT CAGAAAGACA

1951 GTATGCAAGA TGAGTCAAGT CAGACTTCAT TACAGAAAGA GATTAGTACT

2001 GAAGAGCAGC TAAGGCGCCT GCAAGAGGAG AAGCTTTGCA AAATCTGTAT

Fig. 15 (Page 2 of 3)

2051 GGATAGAAAT ATTGCTATCG TTTTTGTTCC TTGTGGACAT CTAGTCACTT

2101 GTAAACAATG TGCTGAAGCA GTTGACAAGT GTCCCATGTG CTACACAGTC

2151 ATTACTTTCA AGCAAAAAAT TTTTATGTCT TAATCTAACT CTATAGTAGG

2201 CATGTTATGT TGTTCTTATT ACCCTGATTG AATGTGTGAT GTGAACTGAC

2251 TTTAAGTAAT CAGGATTGAA TTCCATTAGC ATTTGCTACC AAGTAGGAAA

2301 AAAAATGTAC ATGGCAGTGT TTTAGTTGGC AATATAATCT TTGAATTTCT

2351 TGATTTTTCA GGGTATTAGC TGTATTATCC ATTTTTTTTA CTGTTATTTA

2401 ATTGAAACCA TAGACTAAGA ATAAGAAGCA TCATACTATA ACTGAACACA

2451 ATGTGTATTC ATAGTATACT GATTTAATTT CTAAGTGTAA GTGAATTAAT

2501 CATCTGGATT TTTTATTCTT TTCAGATAGG CTTAACAAAT GGAGCTTTCT

2551 GTATATAAAT GTGGAGATTA GAGTTAATCT CCCCAATCAC ATAATTTGTT

2601 TTGTGTGAAA AAGGAATAAA TTGTTCCATG CTGGTGGAAA GATAGAGATT

2651 GTTTTTAGAG GTTGGTTGTT GTGTTTTAGG ATTCTGTCCA TTTTCTTTTA

2701 AAGTTATAAA CACGTACTTG TGCGAATTAT TTTTTTAAAG TGATTTGCCA

2751 TTTTTGAAAG CGTATTTAAT GATAGAATAC TATCGAGCCA ACATGTACTG

2801 ACATGGAAAG ATGTCAAAGA TATGTTAAGT GTAAAATGCA AGTGGCAAAA

2851 CACTATGTAT AGTCTGAGCC AGATCAAAGT ATGTATGTTT TTAATATGCA

2901 TAGAACAAAA GATTTGGAAA GATATACACC AAACTGTTAA ATGTGGTTTC

2951 TCTTCGGGGA GGGGGGGATT GGGGGAGGGG CCCCATAGGG GTTTTATAGG

Fig. 15 (Page 3 of 3)

1 TTGCTCTGTC ACCCAGTTTG GAGTGCAGTT ATGCAGTCTC ACACTGCAAG

51 CTCTGCCTCA TGGGCTCAAG TGAACCTCCT GCCTCAGCCT CTCAAGTAGC

101 TGGGACCACA GGCAGGTGCC ACCATGTCTG GCTAATTTTT GAGTTTCTTT

151 GTAGAGATGG TGTTTTGCCA AGTCACCCAG TTTGAGGCTG GTCTCAAACA

201 CCTGGGCTCA AGCAATCCAT CTACCTCAGC CTCCCAAAGT GCTGGGATTA

251 CAGGAGTGAG CCATGGCATG AGGCCTTGTG GGGTGTCTCT TTTAAATGAA

301 AGCATACTCT GTTTACGTAT TTGATATGAA GGAATATCCT TCCTTTCCAC

351 AAAGACAAAA ATTATCCTAT TTTTCTCAAA ACATATGTCC TTTTTCTCTA

401 CTTTTCATTT TTGTTACTTT TGATGGACAC ATGTGTTACA TTGATTTCAC

451 TTTCTCATAA TTCTGCTGTA AGAAAAACAA TAGTGCCAGT TCAATGACAA

501 ATAGCAACAG TCTGTTATTG CTAGACTGTT ACTGTTAGTG GAGACTACCA

551 GAACAGTCAG TCCCAGTGTC AGGGAATCAA AGAGAACATG TTCCCTCTCT

601 AAAGGGCACA GCTGCTGCTC AGCTTTAGCT GATTGCTGCC CTGCAGGACT

651 ATAGGCCCAG TGTTGCTAGA TCTTTTGATG TTTCAAGAGA AGCTTGGAAT

701 CTAGAATGTG ATGGGAAGTC TCTTACATTT AAACATGTTG GCAATTAATG

Fig. 16 (Page 1 of 9)

751 GTAAGATTTA AAAATACTGT GGTCCAAGAA AAAAATGGAT TTGGAAACTG

801 GATTAAATTC AAATGAGGCA TGCAGATTAA TCTACAGCAT GGTACAATGT

851 GAATTTTCTG GTTTCTTTAA TTGCACTGTA ATTAGGTAAG ATGTTAGCTT

901 TGGGGAAGCT AAGTGCAGAG TATGCAGAAA CTATTATTTT TGTAAGTTTT

951 CTCTAAGTAT AAATAAATTT CAAAATAAAA ATAAAAACTT AGTAAAGAAC

1001 TATAATGCAA TTCTATGTAA GCCAAACATA ATATGTCTTC CAGTTTGAAA

1051 CCTCTGGGTT TTATTTTATT TTATTTTATT TTTGAGACAG AGTCTTGCTG

1101 TGTCACCCAG GCTGGAGTGT AGTGGCACTA TTTCGGCCCA CTGCAACCTC

1151 CACCTCCCAG GCTCAAATGA TTCTCCTGCC TCAGCCTCCG GAGTAGCTGG

1201 GATTACAGGC GCGTACCACC ACACCCAGCT AATTTTTGTA TTTTTAGTAG

1251 AGATGGGGTT TCACCATTTT GGCCAGGCTG GTTTTGAACT CCTGACCTCA

1301 AGTGATCCAC TTGTCTTGGC CTCCCAAAAT GCTGGGATTA CAGGCGTGAG

1351 CCACTGCACC AGGCAGAGGC CTCTGTTTTT TATCTCTTTT TGGCCTCTAC

1401 AGTGCCTAGT AAAGCACCTG ATACATGGTA AACGATCAGT AATTACTAGT

1451 ACTCTATTTT GGAGAAAATG ATTTTTTAAA AAGTCATTGT GTTCCATCCA

Fig. 16 (Page 2 of 9)

1501 TGAGTCGTTT GAGTTTTAAA ACTGTCTTTT TGTTTGTTTT TGAACAGGTT

1551 TACAAAGGAG GAAAACGACT TCTTCTAGAT TTTTTTTTCA GTTTCTTCTA

1601 TAAATCAAAA CATCTCAAAA TGGAGACCTA AAATCCTTAA AGGGACTTAG

1651 TCTAATCTCG GGAGGTAGTT TTGTGCATGG GTAAACAAAT TAAGTATTAA

1701 CTGGTGTTTT ACTATCCAAA GAATGCTAAT TTTATAAACA TGATCGAGTT

1751 ATATAAGGTA TACCATAATG AGTTTGATTT TGAATTTGAT TTGTGGAAAT

1801 AAAGGAAAAG TGATTCTAGC TGGGGCATAT TGTTAAAGCA TTTTTTTCAG

1851 AGTTGGCCAG GCAGTCTCCT ACTGGCACAT TCTCCCATTA TGTAGAATAG

1901 AAATAGTACC TGTGTTTGGG AAAGATTTTA AAATGAGTGA CAGTTATTTG

1951 GAACAAAGAG CTAATAATCA ATCCACTGCA AATTAAAGAA ACATGCAGAT

2001 GAAAGTTTTG ACACATTAAA ATACTTCTAC AGTGACAAAG AAAAATCAAG

2051 AACAAAGCTT TTTGATATGT GCAACAAATT TAGAGGAAGT AAAAAGATAA

2101 ATGTGATGAT TGGTCAAGAA ATTATCCAGT TATTTACAAG GCCACTGATA

2151 TTTTAAACGT CCAAAAGTTT GTTTAAATGG GCTGTTACCG CTGAGAATGA

2201 TGAGGATGAG AATGATGGTT GAAGGTTACA TTTTAGGAAA TGAAGAAACT

2251 TAGAAAATTA ATATAAAGAC AGTGATGAAT ACAAAGAAGA

Fig. 16 (Page 3 of 9)

TTTTTATAAC

2301 AATGTGTAAA ATTTTTGGCC AGGGAAAGGA ATATTGAAGT
TAGATACAAT

2351 TACTTACCTT TGAGGGAAAT AATTGTTGGT AATGAGATGT
GATGTTTCTC

2401 CTGCCACCTG GAAACAAAGC ATTGAAGTCT GCAGTTGAAA
AGCCCAACGT

2451 CTGTGAGATC CAGGAAACCA TGCTTGCAAA CCACTGGTAA
AAAAAAAAAA

2501 AAAAAAAAAA AAAGCCACAG TGACTTGCTT ATTGGTCATT
GCTAGTATTA

2551 TCGACTCAGA ACCTCTTTAC TAATGGCTAG TAAATCATAA
TTGAGAAATT

2601 CTGAATTTTG ACAAGGTCTC TGCTGTTGAA ATGGTAAATT
TATTATTTTT

2651 TTTGTCATGA TAAATTCTGG TTCAAGGTAT GCTATCCATG
AAATAATTTC

2701 TGACCAAAAC TAAATTGATG CAATTTGATT ATCCATCTTA
GCCTACAGAT

2751 GGCATCTGGT AACTTTTGAC TGTTTTAAAA AATAAATCCA
CTATCAGAGT

2801 AGATTTGATG TTGGCTTCAG AAACATTTAG AAAAACAAAA
GTTCAAAAAT

2851 GTTTTCAGGA GGTGATAAGT TGAATAACTC TACAATGTTA
GTTCTTTGAG

2901 GGGGACAAAA AATTTAAAAT CTTTGAAAGG TCTTATTTTA
CAGCCATATC

2951 TAAATTATCT TAAGAAAATT TTTAACAAAG GGAATGAAAT
ATATATCATG

3001 ATTCTGTTTT TCCAAAAGTA ACCTGAATAT AGCAATGAAG
TTCAGTTTTG

Fig. 16 (Page 4 of 9)

3051 TTATTGGTAG TTTGGGCAGA GTCTCTTTTT GCAGCACCTG TTGTCTACCA

3101 TAATTACAGA GGACATTTCC ATGTTCTAGC CAAGTATACT ATTAGAATAA

3151 AAAAACTTAA CATTGAGTTG CTTCAACAGC ATGAAACTGA GTCCAAAAGA

3201 CCAAATGAAC AAACACATTA ATCTCTGATT ATTTATTTTA AATAGAATAT

3251 TTAATTGTGT AAGATCTAAT AGTATCATTA TACTTAAGCA ATCATATTCC

3301 TGATGATCTA TGGGAAATAA CTATTATTTA ATTAATATTG AAACCAGGTT

3351 TTAAGATGTG TTAGCCAGTC CTGTTACTAG TAAATCTCTT TATTTGGAGA

3401 GAAATTTTAG ATTGTTTTGT TCTCCTTATT AGAAGGATTG TAGAAAGAAA

3451 AAAATGACTA ATTGGAGAAA AATTGGGGAT ATATCATATT TCACTGAATT

3501 CAAAATGTCT TCAGTTGTAA ATCTTACCAT TATTTTACGT ACCTCTAAGA

3551 AATAAAAGTG CTTCTAATTA AAATATGATG TCATTAATTA TGAAATACTT

3601 CTTGATAACA GAAGTTTTAA AATAGCCATC TTAGAATCAG TGAAATATGG

3651 TAATGTATTA TTTTCCTCCT TTGAGTNAGG TCTTGTGCTT TTTNTTCCTG

3701 GCCACTAAAT NTCACCATNT CCAANAAGCA AANTAAACCT ATTCTGAATA

3751 TTTTTGCTGT GAAACACTTG NCAGCAGAGC TTTCCCNCCA TGNNAGAAGC

Fig. 16 (Page 5 of 9)

3801 TTCATGAGTC ACACATTACA TCTTTGGGTT GATTGAATGC
CACTGAAACA

3851 TTTCTAGTAG CCTGGAGNAG TTGACCTACC TGTGGAGATG
CCTGCCATTA

3901 AATGGCATCC TGATGGCTTA ATACACATCA CTCTTCTGTG
NAGGGTTTTA

3951 ATTTTCAACA CAGCTTACTC TGTAGCATCA TGTTTACATT
GTATGTATAA

4001 AGATTATACN AAGGTGCAAT TGTGTATTTC TTCCTTAAAA
TGTATCAGTA

4051 TAGGATTTAG AATCTCCATG TTGAAACTCT AAATGCATAG
AAATAAAAAT

4101 AATAAAAAAT TTTTCATTTT GGCTTTTCAG CCTAGTATTA
AAACTGATAA

4151 AAGCAAAGCC ATGCACAAAA CTACCTCCCT AGAGAAAGGC
TAGTCCCTTT

4201 TCTTCCCCAT TCATTTCATT ATGAACATAG TAGAAAACAG
CATATTCTTA

4251 TCAAATTTGA TGAAAAGCGC CAACACGTTT GAACTGAAAT
ACGACTTGTC

4301 ATGTGAACTG TACCGAATGT CTACGTATTC CACTTTTCCT
GCTGGGGTTC

4351 CTGTCTCAGA AAGGAGTCTT GCTCGTGCTG GTTTCTATTA
CACTGGTGTG

4401 AATGACAAGG TCAAATGCTT CTGTTGTGGC CTGATGCTGG
ATAACTGGAA

4451 AAGAGGAGAC AGTCCTACTG AAAAGCATAA AAAGTTGTAT
CCTAGCTGCA

4501 GATTCGTTCA GAGTCTAAAT TCCGTTAACA ACTTGGAAGC
TACCTCTCAG

4551 CCTACTTTTC CTTCTTCAGT AACACATTCC ACACACTCAT

Fig. 16 (Page 6 of 9)

TACTTCCGGG

4601 TACAGAAAAC AGTGGATATT TCCGTGGCTC TTATTCAAAC TCTCCATCAA

4651 ATCCTGTAAA CTCCAGAGCA AATCAAGAAT TTTCTGCCTT GATGAGAAGT

4701 TCCTACCCCT GTCCAATGAA TAACGAAAAT GCCAGATTAC TTACTTTTCA

4751 GACATGGCCA TTGACTTTTC TGTCGCCAAC AGATCTGGCA CGAGCAGGCT

4801 TTTACTACAT AGGACCTGGA GACAGAGTGG CTTGCTTTGC CTGTGGTGGA

4851 AAATTGAGCA ATTGGGAACC GAAGGATAAT GCTATGTCAG AACACCTGAG

4901 ACATTTTCCC AAATGCCCAT TTATAGAAAA TCAGCTTCAA GACACTTCAA

4951 GATACACAGT TTCTAATCTG AGCATGCAGA CACATGCAGC CCGCTTTAAA

5001 ACATTCTTTA ACTGGCCCTC TAGTGTTCTA GTTAATCCTG AGCAGCTTGC

5051 AAGTGCGGGT TTTTATTATG TGGGTAACAG TGATGATGTC AAATGCTTTT

5101 GCTGTGATGG TGGACTCAGG TGTTGGGAAT CTGGAGATGA TCCATGGGTT

5151 CAACATGCCA AGTGGTTTCC AAGGTGTGAG TACTTGATAA GAATTAAAGG

5201 ACAGGAGTTC ATCCGTCAAG TTCAAGCCAG TTACCCTCAT CTACTTGAAC

5251 AGCTGCTATC CACATCAGAC AGCCCAGGAG ATGAAAATGC AGAGTCATCA

5301 ATTATCCATT TTGAACCTGG AGAAGACCAT TCAGAAGATG CAATCATGAT

Fig. 16 (Page 7 of 9)

5351 GAATACTCCT GTGATTAATG CTGCCGTGGA AATGGGCTTT AGTAGAAGCC

5401 TGGTAAAACA GACAGTTCAG AGAAAAATCC TAGCAACTGG AGAGAATTAT

5451 AGACTAGTCA ATGATCTTGT GTTAGACTTA CTCAATGCAG AAGATGAAAT

5501 AAGGGAAGAG GAGAGAGAAA GAGCAACTGA GGAAAAAGAA TCAAATGATT

5551 TATTATTAAT CCGGAAGAAT AGAATGGCAC TTTTTCAACA TTTGACTTGT

5601 GTAATTCCAA TCCTGGATAG TCTACTAACT GCCGGAATTA TTAATGAACA

5651 AGAACATGAT GTTATTAAAC AGAAGACACA GACGTCTTTA CAAGCAAGAG

5701 AACTGATTGA TACGATTTTA GTAAAAGGAA ATATTGCAGC CACTGTATTC

5751 AGAAACTCTC TGCAAGAAGC TGAAGCTGTG TTATATGAGC ATTTATTTGT

5801 GCAACAGGAC ATAAAATATA TTCCCACAGA AGATGTTTCA GATCTACCAG

5851 TGGAAGAACA ATTGCGGAGA CTACAAGAAG AAAGAACATG TAAAGTGTGT

5901 ATGGACAAAG AAGTGTCCAT AGTGTTTATT CCTTGTGGTC ATCTAGTAGT

5951 ATGCAAAGAT TGTGCTCCTT CTTTAAGAAA GTGTCCTATT TGTAGGAGTA

6001 CAATCAAGGG TACAGTTCGT ACATTTCTTT CATGAAGAAG AACCAAAACA

6051 TCGTCTAAAC TTTAGAATTA ATTTATTAAA TGTATTATAA CTTTAACTTT

Fig. 16 (Page 8 of 9)

6101 TATCCTAATT TGGTTTCCTT AAAATTTTTA TTTATTTACA ACTCAAAAAA

6151 CATTGTTTTG TGTAACATAT TTATATATGT ATCTAAACCA TATGAACATA

6201 TATTTTTTAG AAACTAAGAG AATGATAGGC TTTTGTTCTT ATGAACGAAA

6251 AAGAGGTAGC ACTACAAACA CAATATTCAA TCAAAATTTC AGCATTATTG

6301 AAATTGTAAG TGAAGTAAAA CTTAAGATAT TTGAGTTAAC CTTTAAGAAT

6351 TTTAAATATT TTGGCATTGT ACTAATACCG GGAACATGAA GCCAGGTGTG

6401 GTGGTATGTG CCTGTAGTCC CAGGCTGAGG CAAGAGAATT ACTTGAGCCC

6451 AGGAGTTTGA ATCCATCCTG GGCAGCATAC TGAGACCCTG CCTTTAAAAA

6501 CAAACAGAAC AAAAACAAAA CACCAGGGAC ACATTTCTCT GTCTTTTTTG

6551 ATCAGTGTCC TATACATCGA AGGTGTGCAT ATATGTTGAA TCACATTTTA

6601 GGGACATGGT GTTTTTATAA AGAATTCTGT GAGAAAAAAT TTAATAAAGC

6651 AACCAAAAAA AAAAAAAAAA

Fig. 16 (Page 9 of 9)